

FIG. 1A

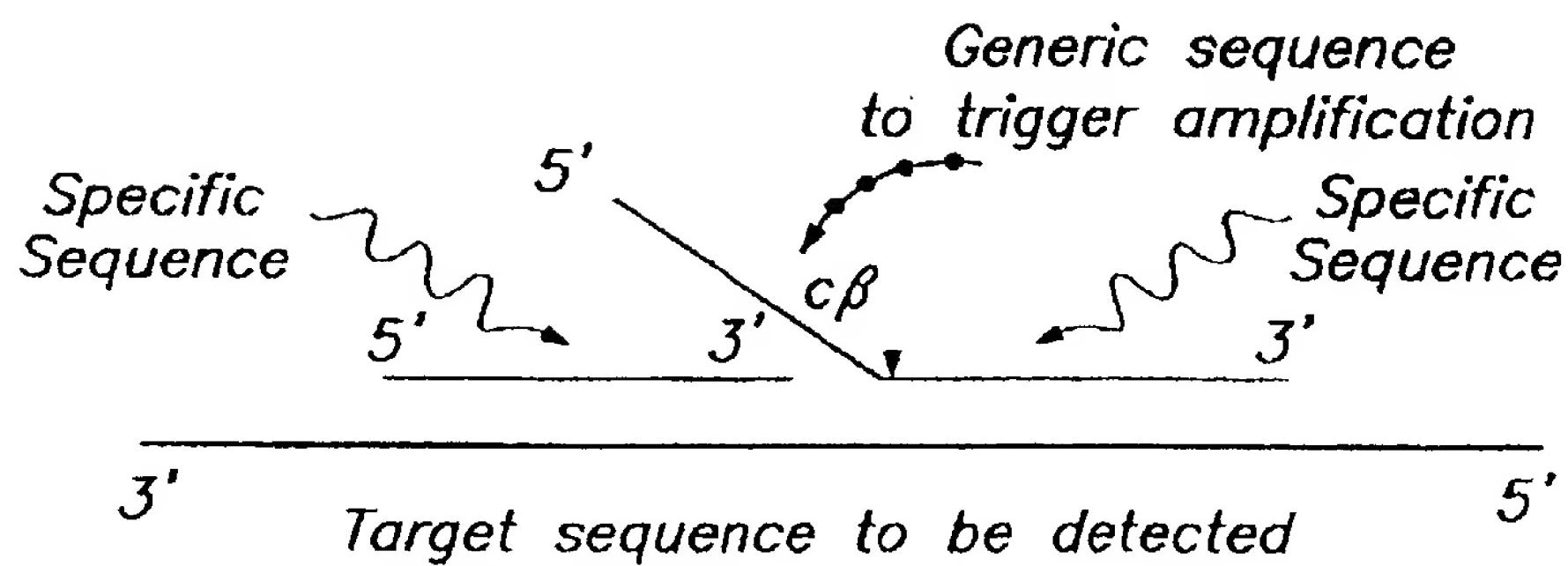


FIG. 1B PART ONE: TRIGGER REACTION

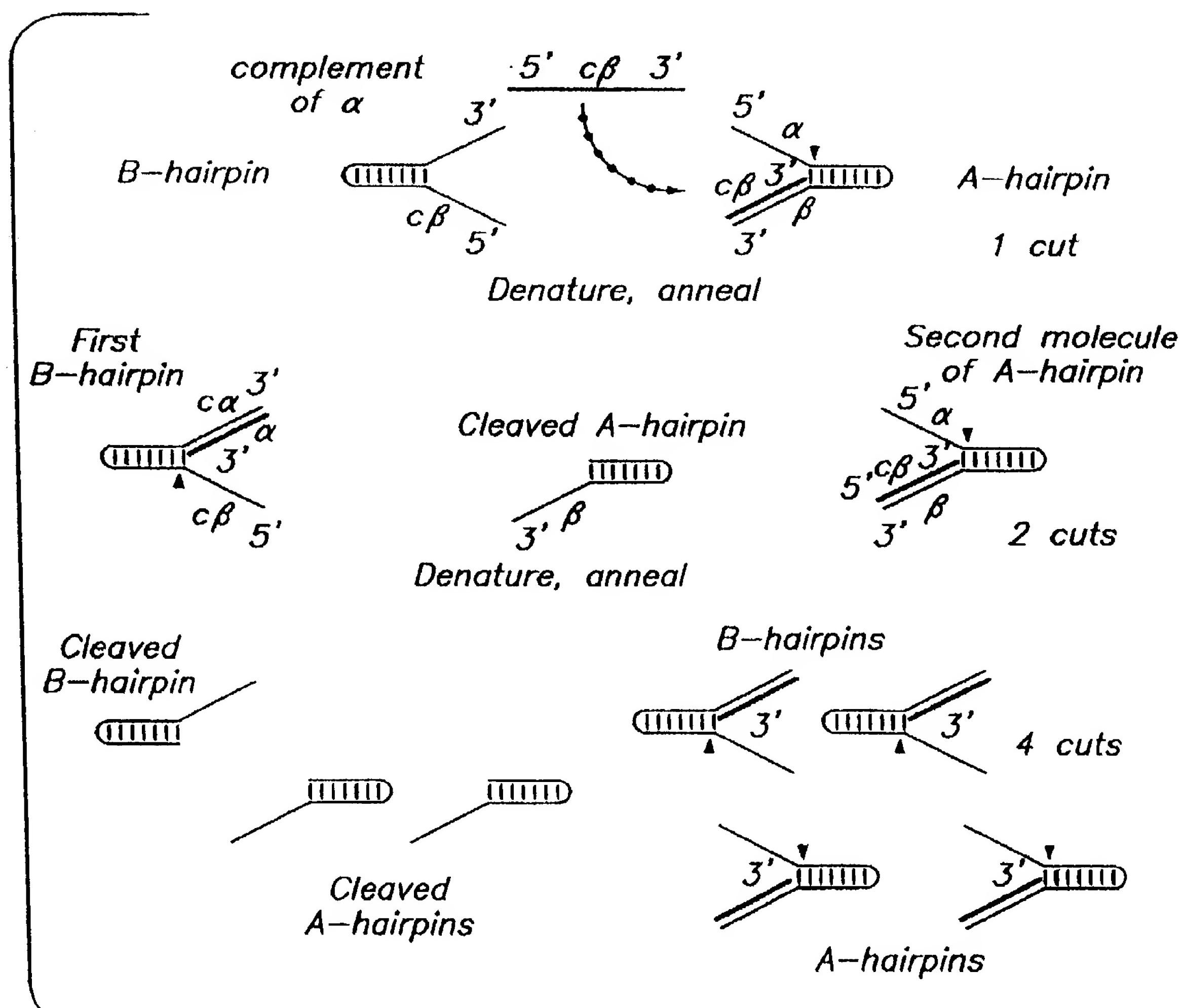


FIG. 1C PART TWO: DETECTION REACTION

FIG. 2A

DHAPTAQ [SEQ ID NO:1] . . . A G . . . G . . . G . . . G . . .
DHAPFL [SEQ ID NO:2] .
DHAPTH [SEQ ID NO:3] . . . G A . . . G . . . G . . . G . . . A . . .

MAJORITY ACCGACCTCTGGCTCACCAAGGGAACGGTGCAGGCTAACGGTT

DINAPTAO	140
DINAPTFL	137
DINAPTR	140

MAGNITUDE CGGGAGGGCTTCAAGGCCGCGGTGCTCGX

CHAPTER	G	A.	A.	207
CHAPTER	A.	T.	T.	204
CHAPTER	A.	T.	A.	210
CHAPTER	G	T.	T.	210

MAJORITY GGGGCTCTCCCCAACGCCCTACGGAGCCTAAGGCCCTAAGGACTTTC
 G. . . GG.
 277
ДИНАРТАО .
 .
 274
ДИНАРТFL .
 .
 280
ДИНАРТН .
 .
 280
MAJORITY GGGGCAAGCTGGCCCTCATCAAGGAGCTGGTGGACCTGCCTGGGGCTTCCC
 .
 347
ДИНАРТАО A.
 .
 344
ДИНАРТFL .
 .
 350
ДИНАРТН .

FIG. 2B

Majority (see 10:71) GAGGGGAGCTGCCATCCTC

CHAPTER [SEQ ID NO:1]
CHAPTER [SEQ ID NO:2]
CHAPTER [SEQ ID NO:3]

MAJORITY ACCGGCAAGGCTTACAGGTCTGGCAAGGGTACCTCA

DNA₁APTAQ .. G..... A..... A. 557
DNA₁PTFL .. AG..... C.G..... 554
DNA₁ASTR .. T..... C..... 550

627 G. . GAG. . T. . GCG. . 628 G. . GAG. . A. . G. . 629 G. . T. . A. . G. . 630 TCG. . A. . A. .

... *cytomegalovirus* *immunity* *infection* *inflammation* *inflammation*

694
691
700

二〇

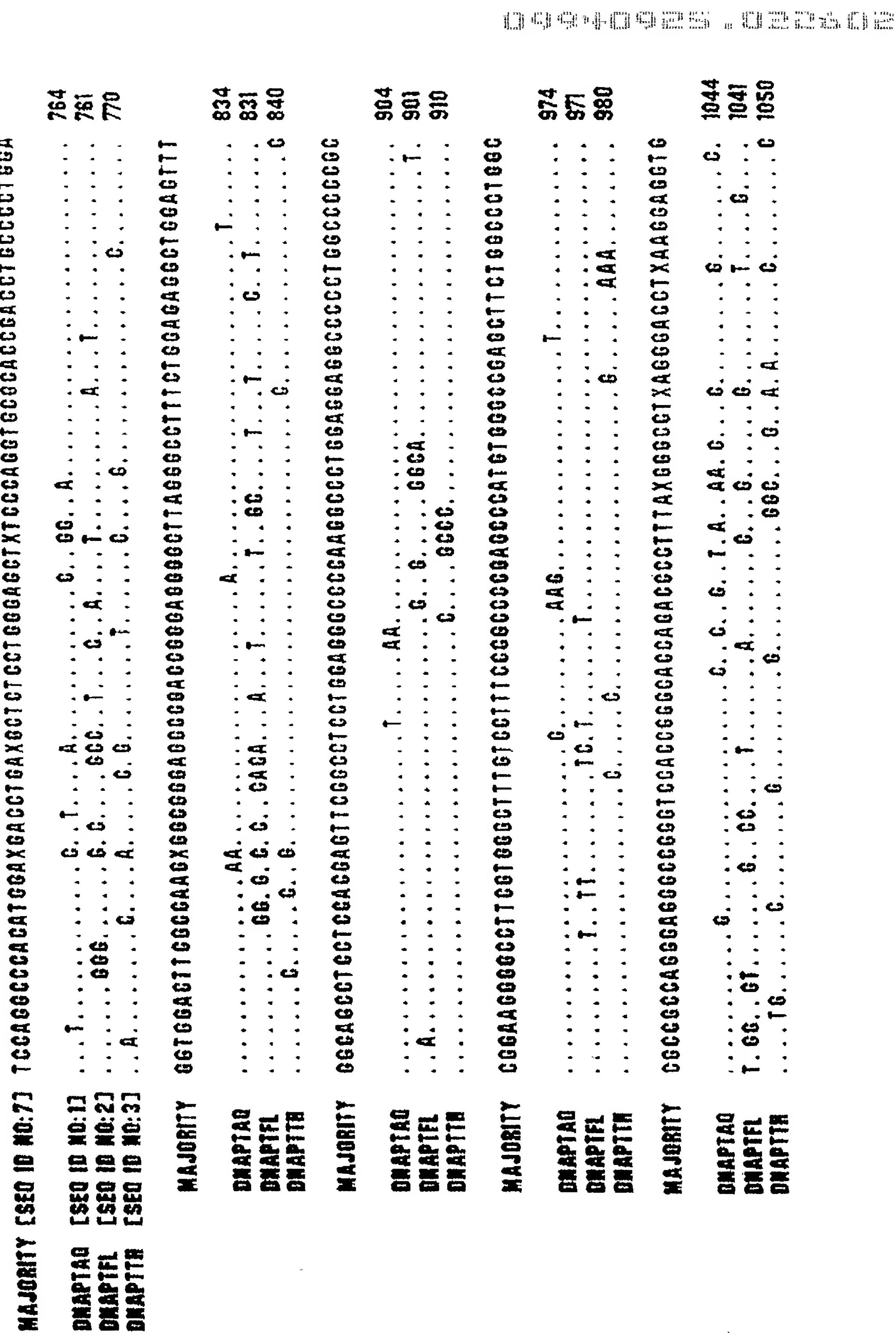


FIG. 2D

FIG. 2E

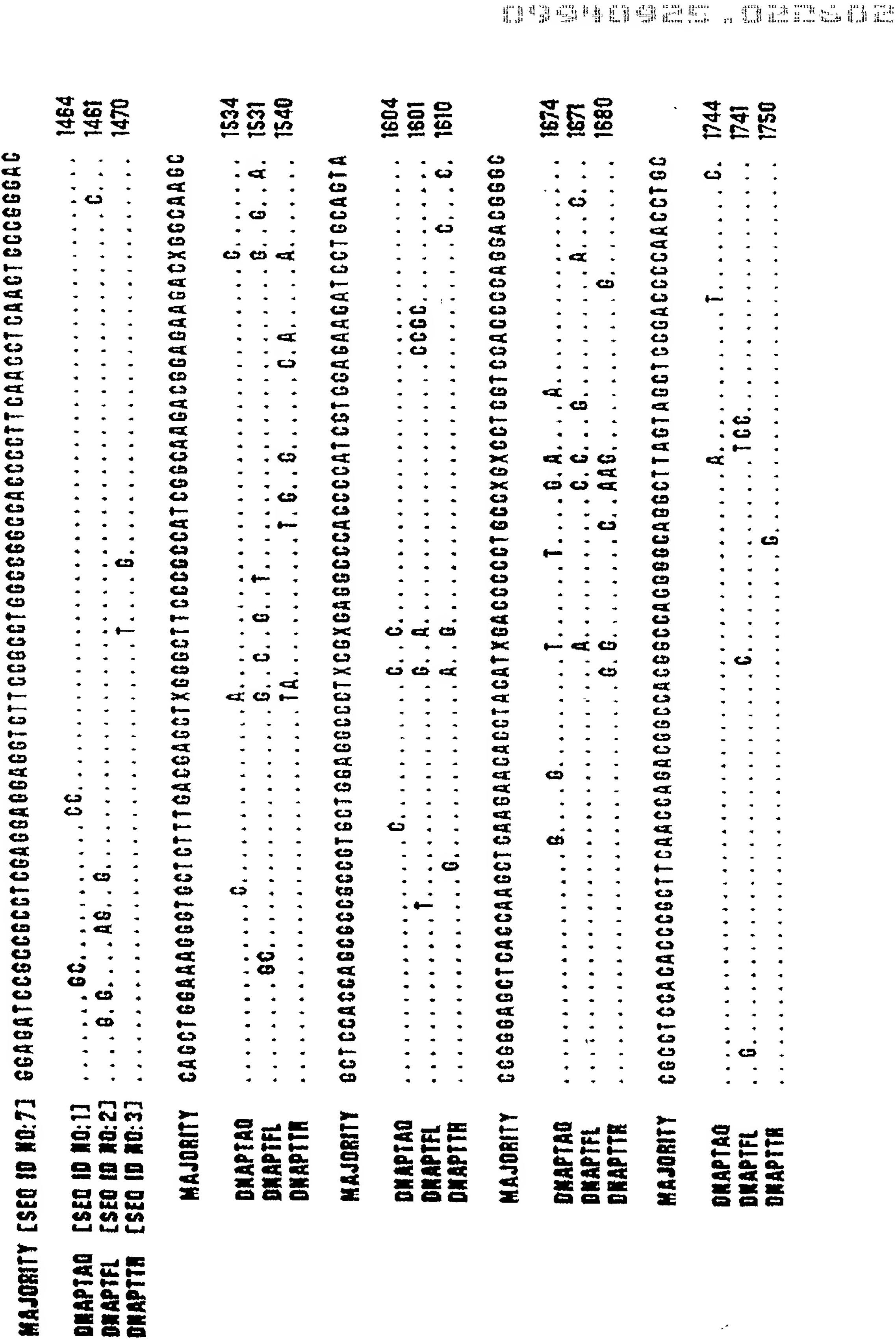


FIG. 2F

MAJORITY [SEQ ID NO:71] AGAACATCCCCCTCCCCAACGGATCCCCGCTTCCCTCCCCGAGGAGGGTGGGT

DNAPTAQ	[SEQ ID NO:1]G.....G.....A.....C.....G.....C.....	1814
DNAPTFI	[SEQ ID NO:2]G.....T.....C.....A.....G.....C.....	1811
DNAPTH	[SEQ ID NO:3]CT.....CT.....G.....T.....G.....C.....	1820

MAJORITY GTCGGTGGCCCTGGACTATAAGCAATAGCCAGCTCCCCGACCTCTCCCCGACGGAAACCTG

DNAPTAQ	A.....	G.....A.....G.....C.....C.....	1884
DNAPTFI	C.....	T.....C.....T.....C.....A.....	1881
DNAPTH	1890

MAJORITY ATCCGGGTCTGGAGGAAGGAGCATGCCACACCCAGGAGGGTGGATGTTCGGGTCCCCGG

DNAPTAQG.....G.....G.....G.....	1954
DNAPTFIT.....T.....T.....T.....	1951
DNAPTHA.....A.....A.....A.....	1960

MAJORITY AGGGCCCTGGACCCCTGATGCCGGGGCCAAAGACCATCAACTTGCGGTCTAACGGCATGTCCCCG

DNAPTAQ	1954
DNAPTFIA.....A.....G.....G.....	2021
DNAPTHA.....A.....G.....G.....	2030

MAJORITY CCACGGCCCTGGACGGCTTGGGCTTGGGGGTGGCCTTCAATTGAGCCCTACTTCCAG

DNAPTAQA.....A.....T.....T.....	2094
DNAPTFIG.....G.....T.....T.....	2091
DNAPTHTA.....G.....A.....A.....	2100

FIG. 2G

MAJORITY [SEQ ID NO:7] AACTTCCCCAACCTGGCCCGATTCAGAACCCTGGATTGAGAAGGAA

DNAPTAQ [SEQ ID NO:13] C.....GG.....A.....A.....G.....A.....A.....

DNAPTFI [SEQ ID NO:2] A.....C.....T.....A.....G.....A.....A.....

DNAPTR [SEQ ID NO:3] G.....A.....G.....A.....G.....A.....A.....

MAJORITY CCCTCTTCCCCCCCCACCTGGCCCGATTCAGAACCCTGGATTGAGAAGGAA

DNAPTAQ C.....A.....A.....G.....G.....A.....A.....A.....

DNAPTFI T.....G.....C.....G.....C.....G.....C.....G.....

DNAPTR AA.....AA.....CA.....CA.....CA.....CA.....A.....

MAJORITY CCCCATGCCCTGAACATGCCGCCACCTCATGAAACCTGCCATGCCAAAGCTC

DNAPTAQ T.....A.....G.....G.....A.....G.....A.....A.....

DNAPTFI G.....G.....G.....G.....G.....G.....G.....G.....

DNAPTR C.....C.....C.....C.....C.....C.....C.....C.....

MAJORITY TTCCCCCCCCXGAGGAAATGGGGCCAGGATGGCTXCAAGGTCCAGGAGGCTGGCTGGGGC

DNAPTAQ A.....GG.....T.....G.....G.....T.....G.....A.....

DNAPTFI T.....G.....G.....G.....G.....G.....G.....G.....

DNAPTR C.....G.....G.....G.....G.....G.....G.....G.....

MAJORITY CCAAGGCCCCAGGXGCTGGCCCTTTGGAAAGGCTCATGGAGGCCCCCTATCCCCCTGGGGCT

DNAPTAQ A.....A.....CC.....GGGG.....G.....G.....G.....

DNAPTFI G.....G.....A.....A.....G.....G.....G.....G.....

DNAPTR G.....G.....A.....A.....G.....G.....G.....G.....

MAJORITY AAGGCCCCCTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCT

DNAPTAQ A.....A.....CC.....GGGG.....G.....G.....G.....

DNAPTFI G.....G.....A.....A.....G.....G.....G.....G.....

DNAPTR G.....G.....A.....A.....G.....G.....G.....G.....

MAJORITY AAGGCCCCCTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCT

DNAPTAQ A.....A.....CC.....GGGG.....G.....G.....G.....

DNAPTFI G.....G.....A.....A.....G.....G.....G.....G.....

DNAPTR G.....G.....A.....A.....G.....G.....G.....G.....

FIG. 2H

MAJORITY [SEQ ID NO:7] GGCGCTGGAGCTGGCGATGGGAAAGACTGGCTCTGGCGAAGCTAG

UNAPTA0	[SEQ ID NO:1]A.....	GA 2499
UNAPTF1	[SEQ ID NO:2]CC..... 2496
UNAPTF1	[SEQ ID NO:3]T.....	GT..... 2505

FIG. 3A

MAJORITY [SEQ ID NO:8]	MXAAML P1FEPKGRVLLVQGHHAYRTFFALKGLTTSRGEPWQAVYGFAKSILKALKEDG. DAUXVVFDAK	H.....H.....V.V.....V.K..F.....	69
TAG PRO	[SEQ ID NO:4]	R.G.....	68
TFL PRO	[SEQ ID NO:5]	70
TTH PRO	[SEQ ID NO:6]	E.....	
MAJORITY	APSFRHEAYAYKAGRAPTPEDFPROLALIKELVOLLGIXRLEVPGYEADDVLATIACKAEKEGYEVRII	A.....A.....S.....A.....F.....V.....F.....	139
TAG PRO	GG.....	138
TFL PRO	140
TTH PRO	
MAJORITY	TADRDLYQLLSDRIAV1HPEGYLITPAWLWEKYGLRPEQWVWYRALXGDPSONLPGVKS! GEKTAXKLIX	B..A.....T..E.....R.....R.....E	209
TAG PRO	...K.....H.....	Y.....A.....I.....A.....I.....	208
TFL PRO	...E.....I.....	Y.....A.....I.....A.....I.....	210
TTH PRO	...V.....V.....	F.....V.....F.....V.....	
MAJORITY	EWGSLEHLLKHLDKVKP. XXREKI XAHMEDIIXLSXXXISXVRTDLPLEVDFAXRREPREGIRAFLERLEF	K.....D.....B.....WD..AK.....K.....R.....	278
TAG PRO	...A.....L.....AI.....L.....	Y.....A.....RK..Q.H.....GR..T..NL.....	277
TFL PRO	...FQH..Q.....SL.....	Q.H.....GR..T..NL.....	280
TTH PRO	...ENV.....ENV.....	L.QG.....L.QG.....	
MAJORITY	GSLIHEFGILEXPKALLEAPWPPPEGAFVGFVLSRPEPMWAELLALAAARXGRVHRAXOPLXGLRDLKEY	K.....D.....G.....PE.YKA.....A.....	348
TAG PROS.....	G.WE..L.....R.....G.....	347
TFL PROG.....A.....	L.SF.....A.....	350
TTH PROA.AP.....	K.....C.D.....A.....A.K.....	

FIG. 3B

MAJORITY [SEQ ID NO:8] RCLLAKDIAVIALREGIDIXPGGDPMLAYLIDPESNTIPCGUARYGGEGWTEADAGEFALLSERBLFXNLXX

TAQ PRO [SEQ ID NO:4] S G . P A A WG 418
TFL PRO [SEQ ID NO:5] I F . E Q K . E 417
TTR PRO [SEQ ID NO:6] S V H L . K 420

MAJORITY RLEGEERILLWLYXEEVKPLSRYVLAHMEATGURLOWAYLOADISLEVAAEIRALEEEVFRALACHPPFHILHSRD

TAQ PRO R R A A 488
TFL PRO K E R EA . V . Q 487
TTR PRO K H L 490

MAJORITY QLERWLFDELGLIPAIQKTEKTGKRSTISAAVILEALRECAHPIWEKILOGYRELTKLKNTYIDPLPXLVHPRTG

TAQ PRO S D 558
TFL PRO Q A K 557
TTR PRO R H V S 560

MAJORITY RLHTRFNOTATAFGRLSSSDPNLQNIPURTPLCQRIRCAFVAEEGWWXLUAVLDYSQIELRVLAHLSGDENL

TAQ PRO I L 628
TFL PRO V V 627
TTR PRO A A 630

MAJORITY I RVFQEGRDIHTOIASWMMF CWPPEAWOPLMRRAAKTIINF GWLYGMSAHLSDELAI PYEEAVAFIERYFO

TAQ PRO E R 698
TFL PRO S S 687
TTR PRO K V 700

FIG. 3C

MAJORITY [SEQ ID NO:8] SFPKVBRWIEKTIFFEGGRACYYETLFGARRYVPBLNARVKSVERAERHAFNNPVPYOGTAADLMNKLAHVKI

TAG PRO [SEQ ID NO:4] E.....
TFL PRO [SEQ ID NO:5] Y..... G.....
TTB PRO [SEQ ID NO:6] K.....

MAJORITY FPRLXEMGARMQLQVHQDELVLEAPKXXRAEXUAALAKEVMEGVYPLAVPLEVENGCGEDWLSAKEK

833
TAG PRO E..... A..... R.....
TFL PRO Q..... L..... D..... R..... W..... Q.....
TTB PRO R..... Q..... A..... E..... A..... KA..... L..... M..... G

831
835

Genes for Wild-Type and Pol(-)DNAP_{Taq}

*Domain
Coding Regions: 5' Nuclease*

FIG. 4A

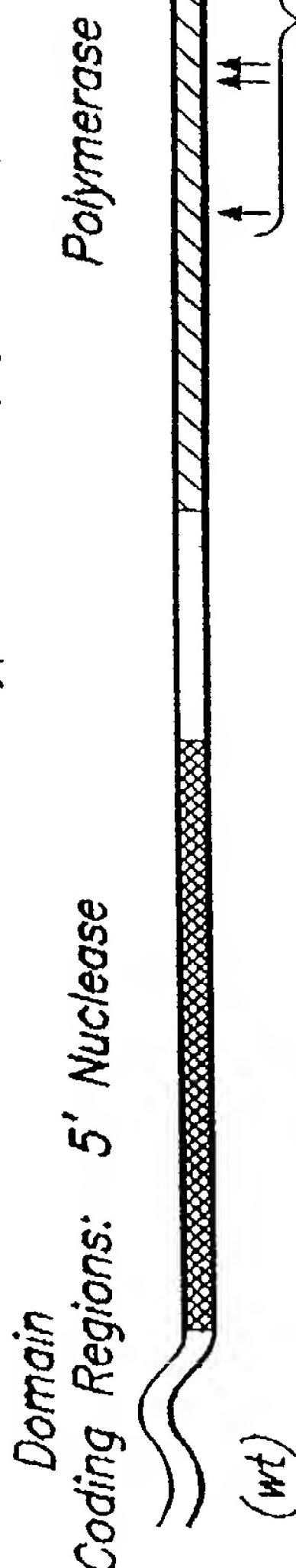


FIG. 4B

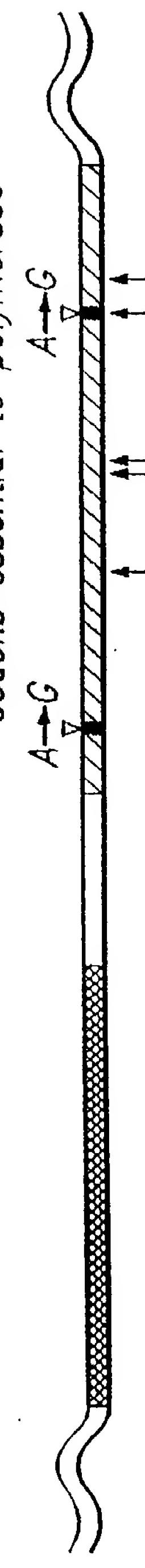


FIG. 4C



FIG. 4D

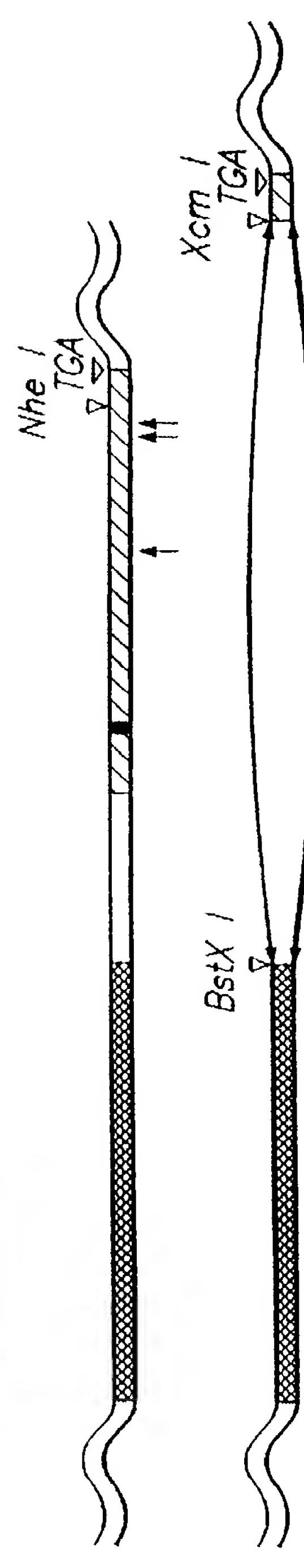


FIG. 4E

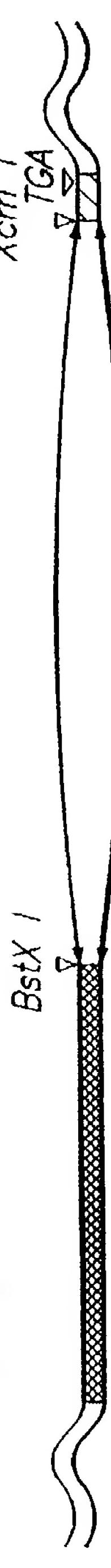


FIG. 4F

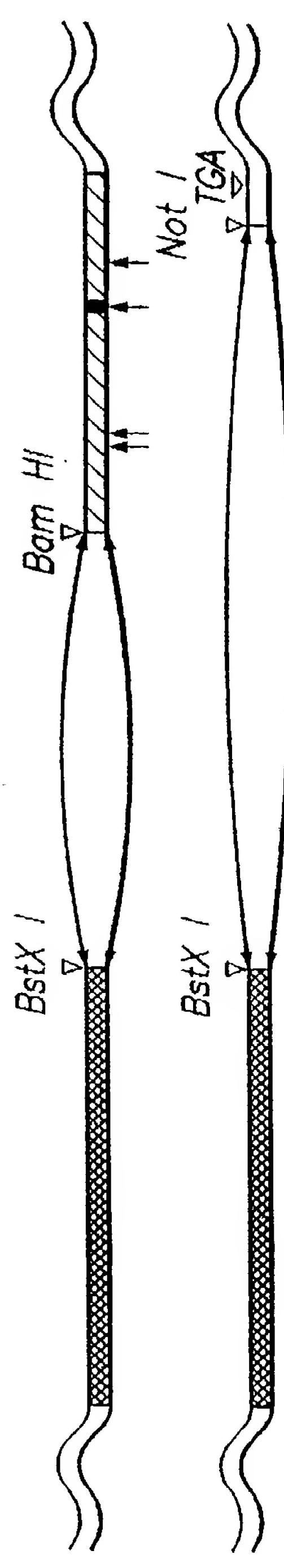
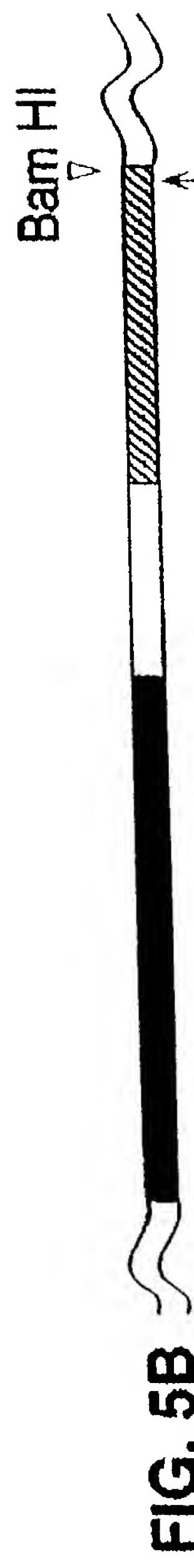
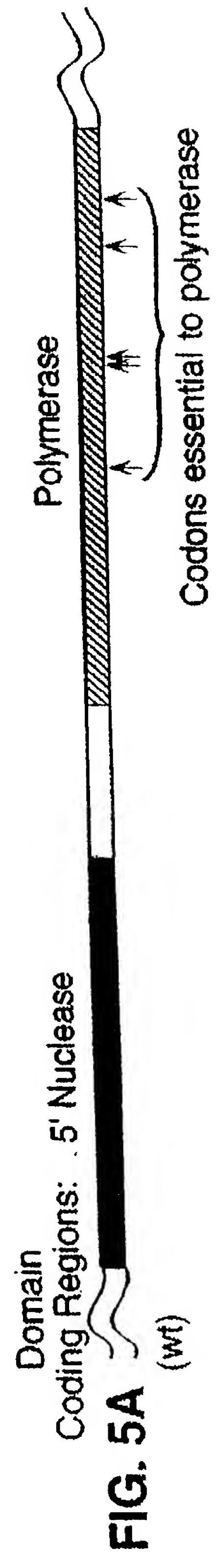


FIG. 4G



Genes for Wild-Type and Pol(-) DNAPT^{fil}



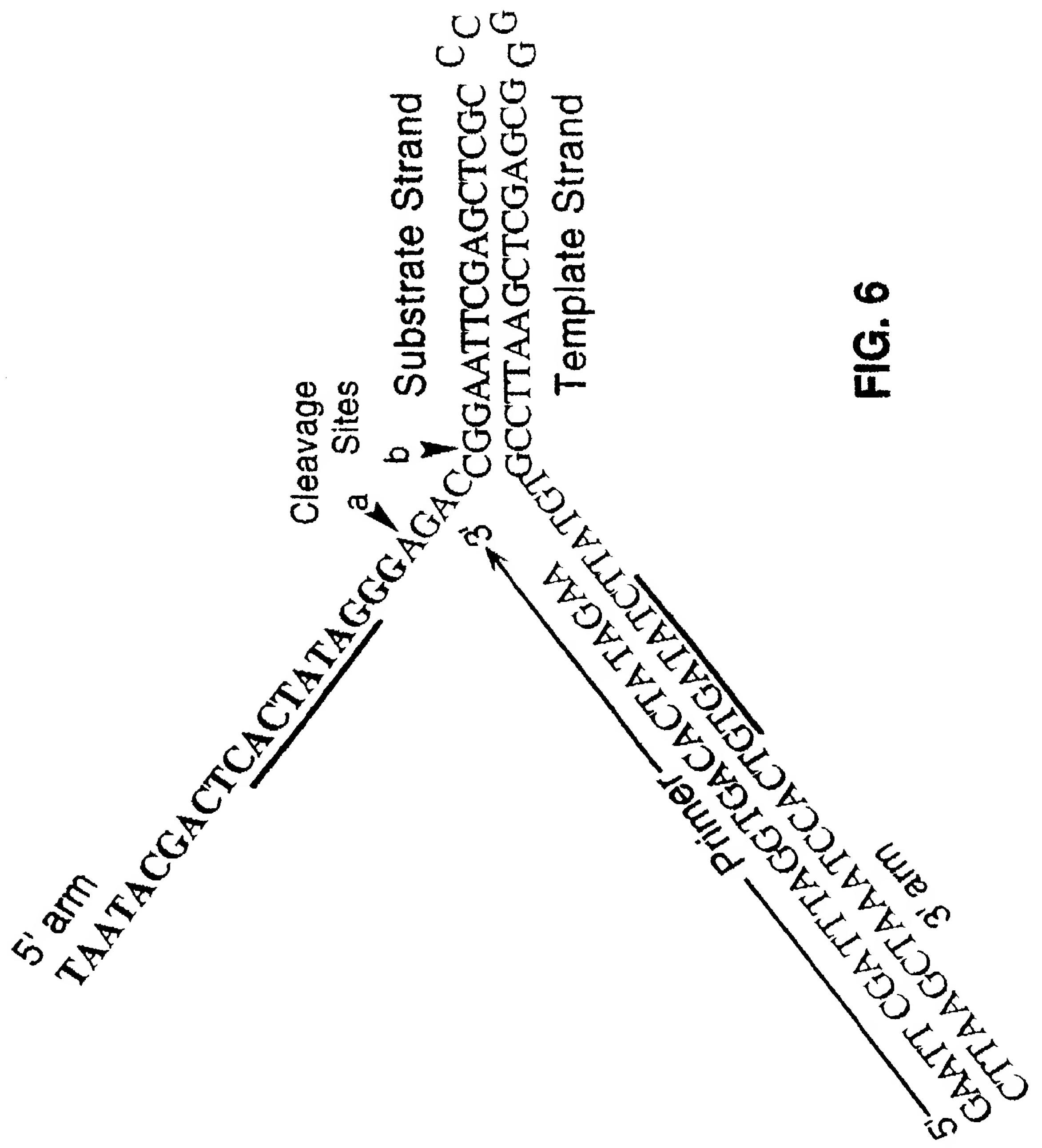


FIG. 6

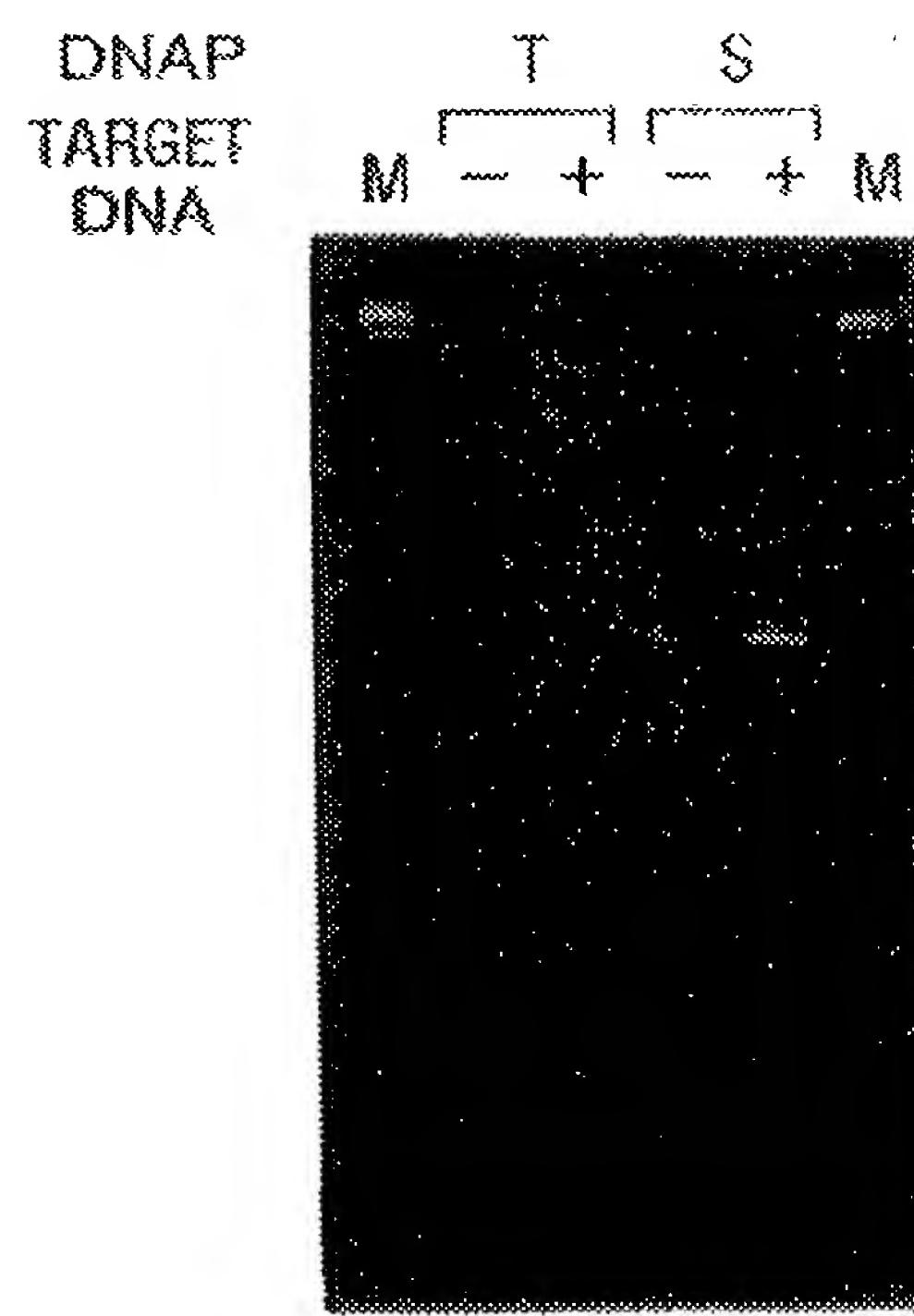


FIG. 7

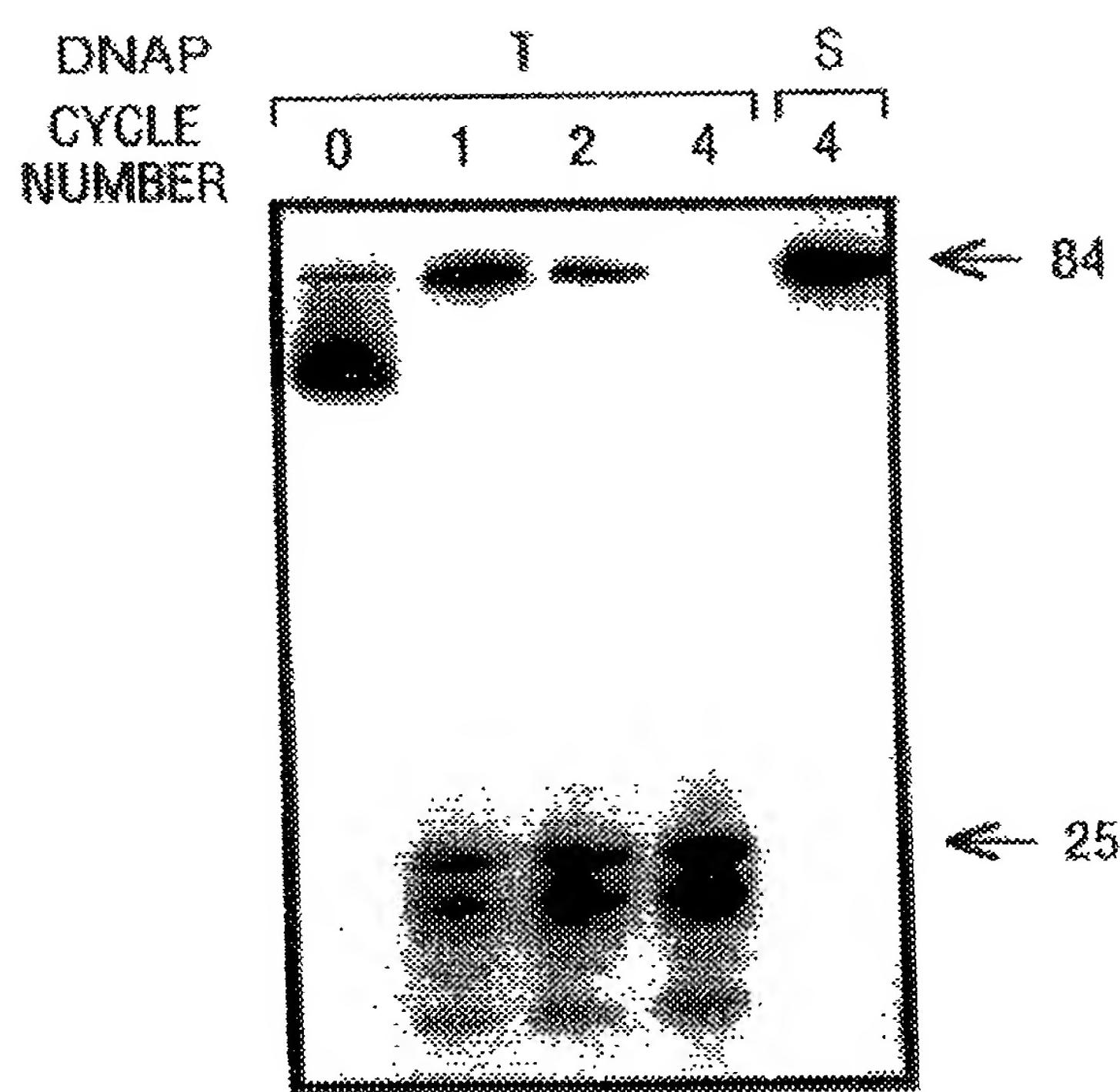


FIG. 8

	1	2	3	4	5	6
DNAP-T	-	*	*	*	*	*
MgCl ₂	*	*	*	*	*	*
dNTPs	*	-	*	-	*	-
Primers	*	*	*	*	*	*

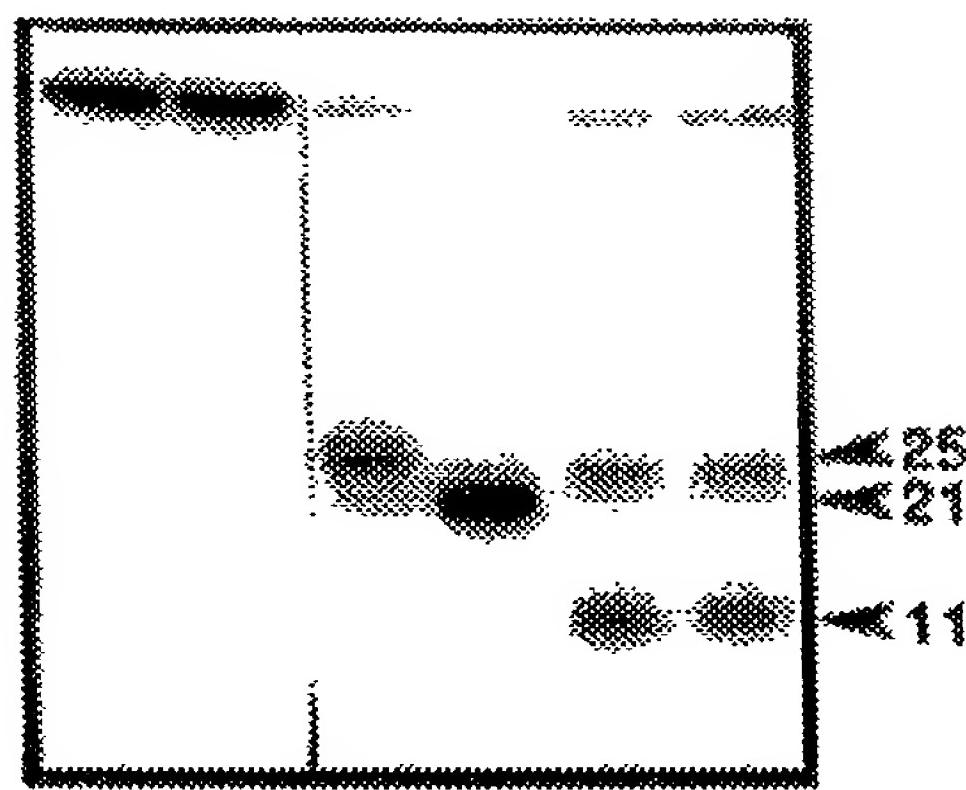


FIG. 9A

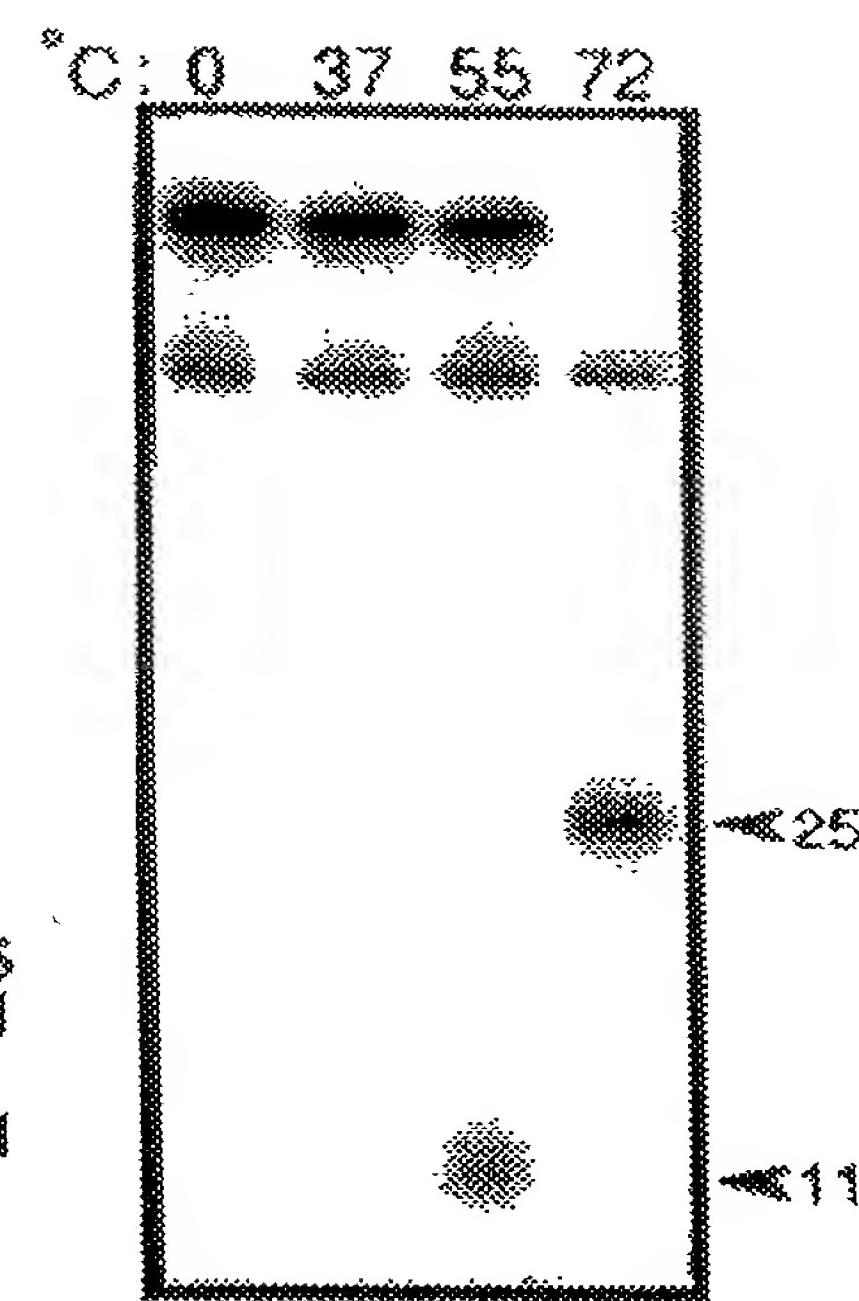


FIG. 9B

CD 43 45 46 47 48 49 50 51 52 53 54

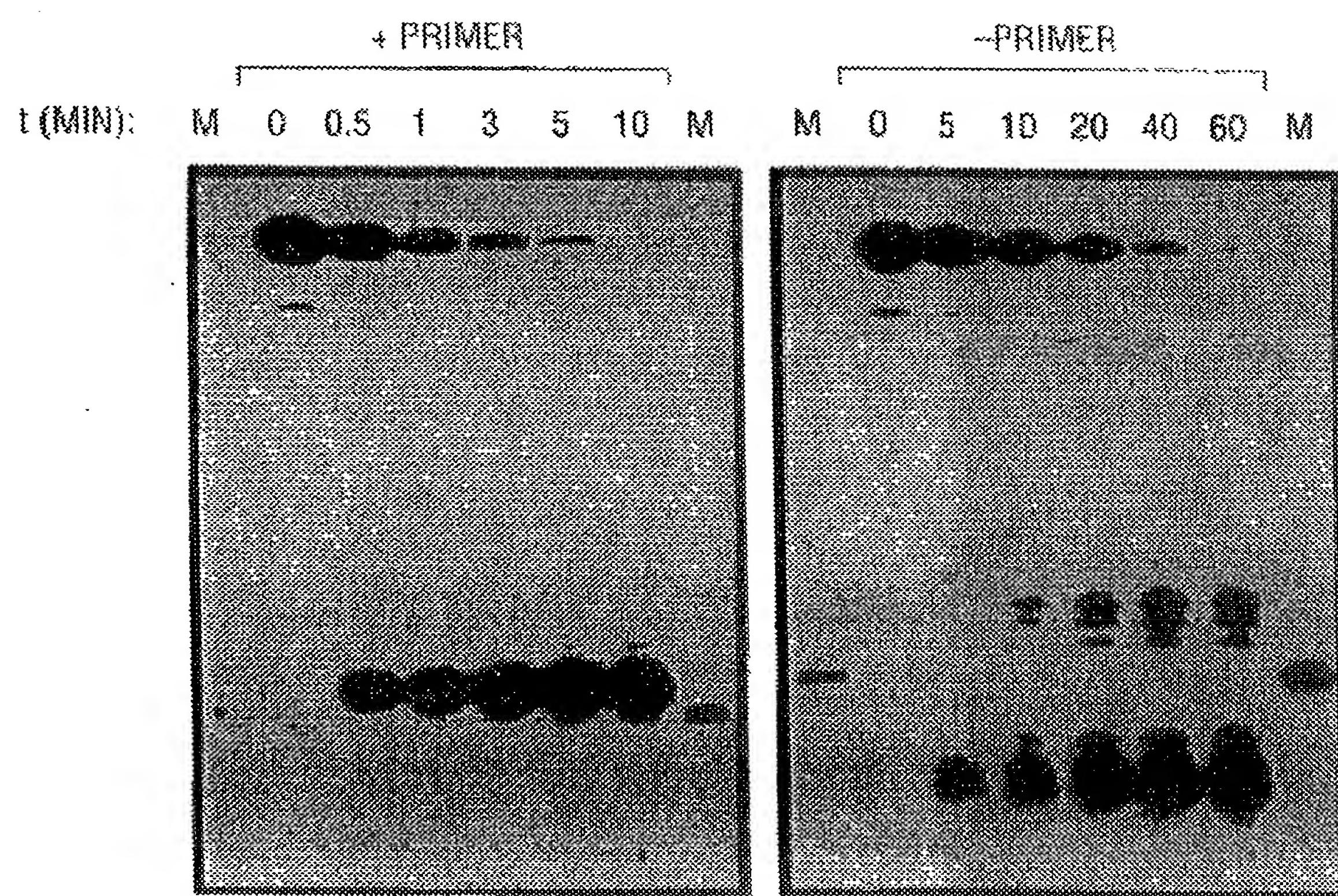


FIG. 10A

FIG. 10B

DNAF: - Pfu Taq T_H T_H T_H - Taq Eco Kpn
 Primer: -- * * * * * * * * * * * *

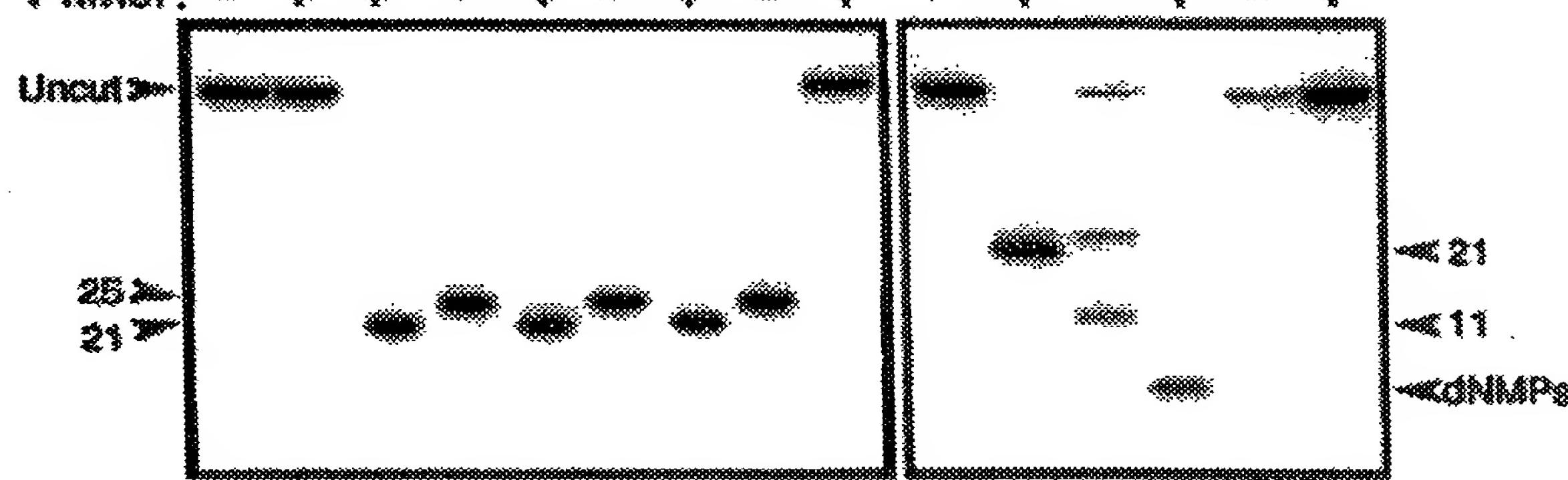
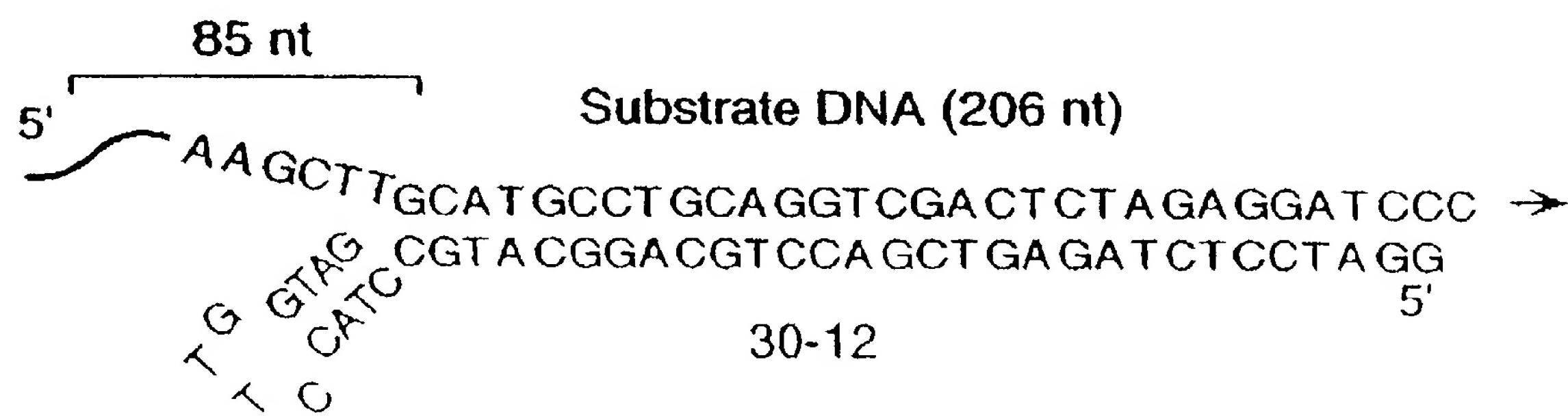
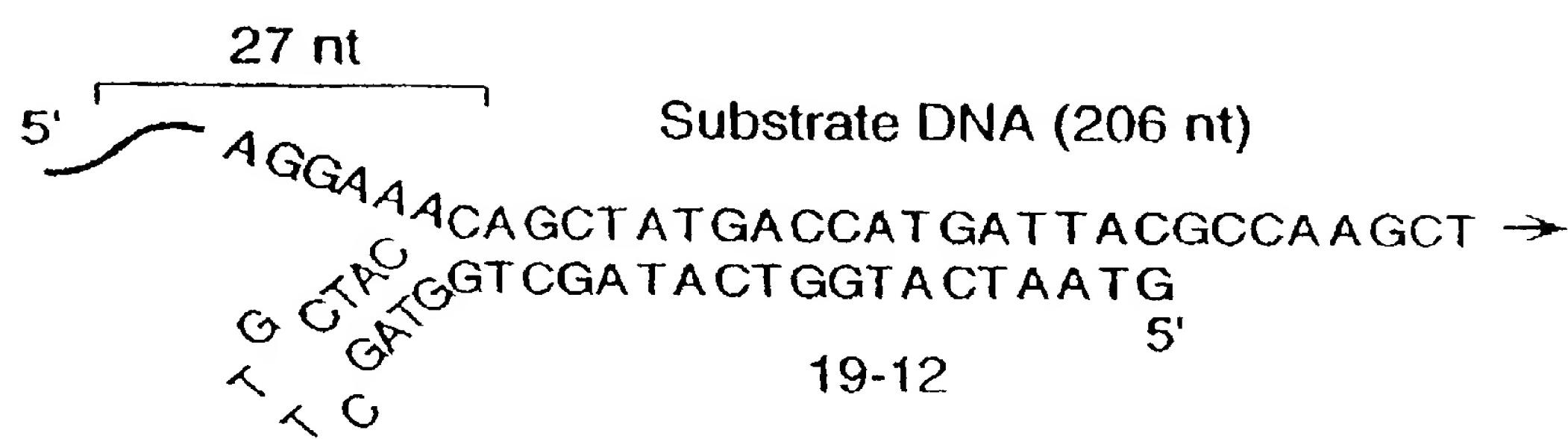


FIG. 11A

FIG. 11B

FIG. 12A



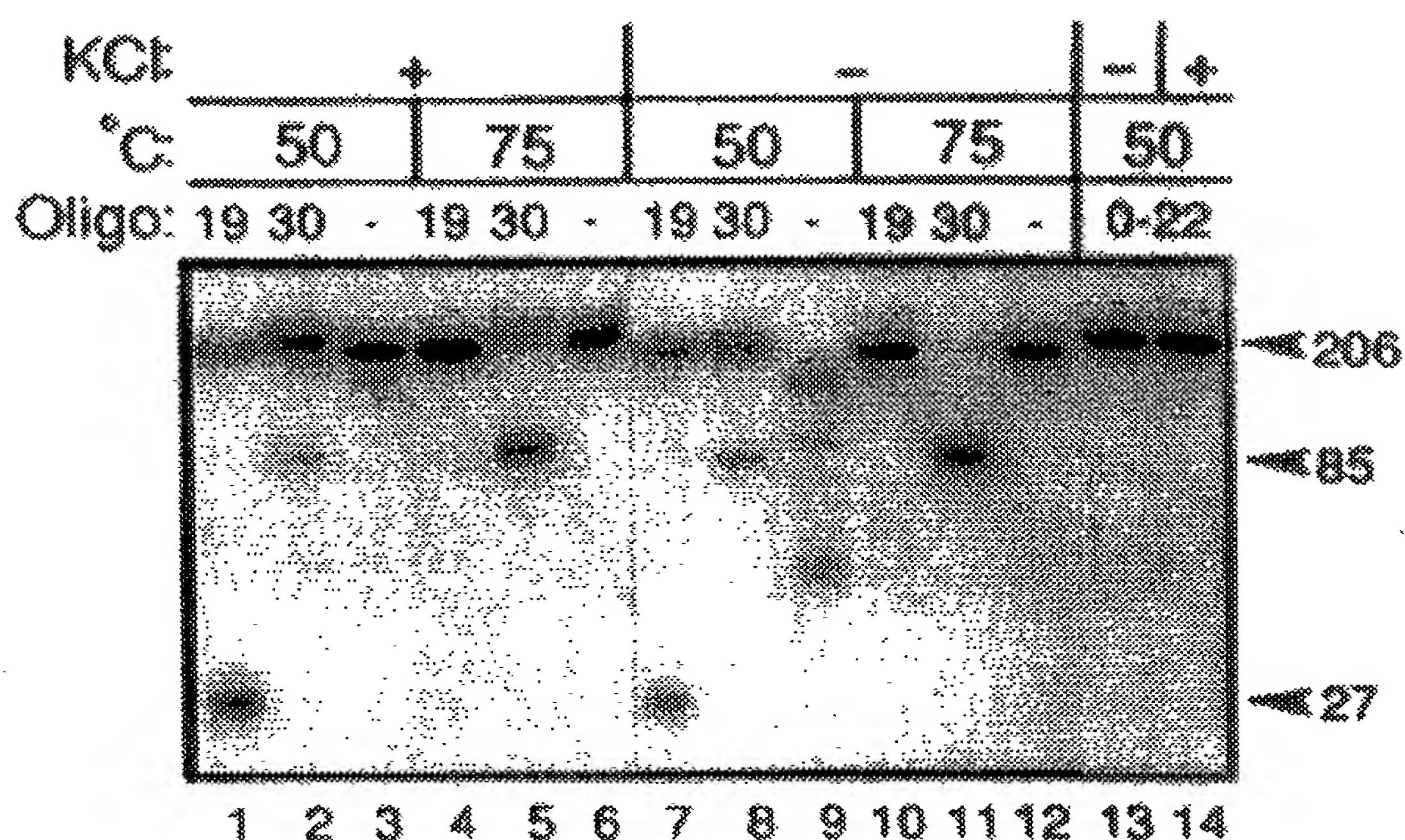


FIG. 12B

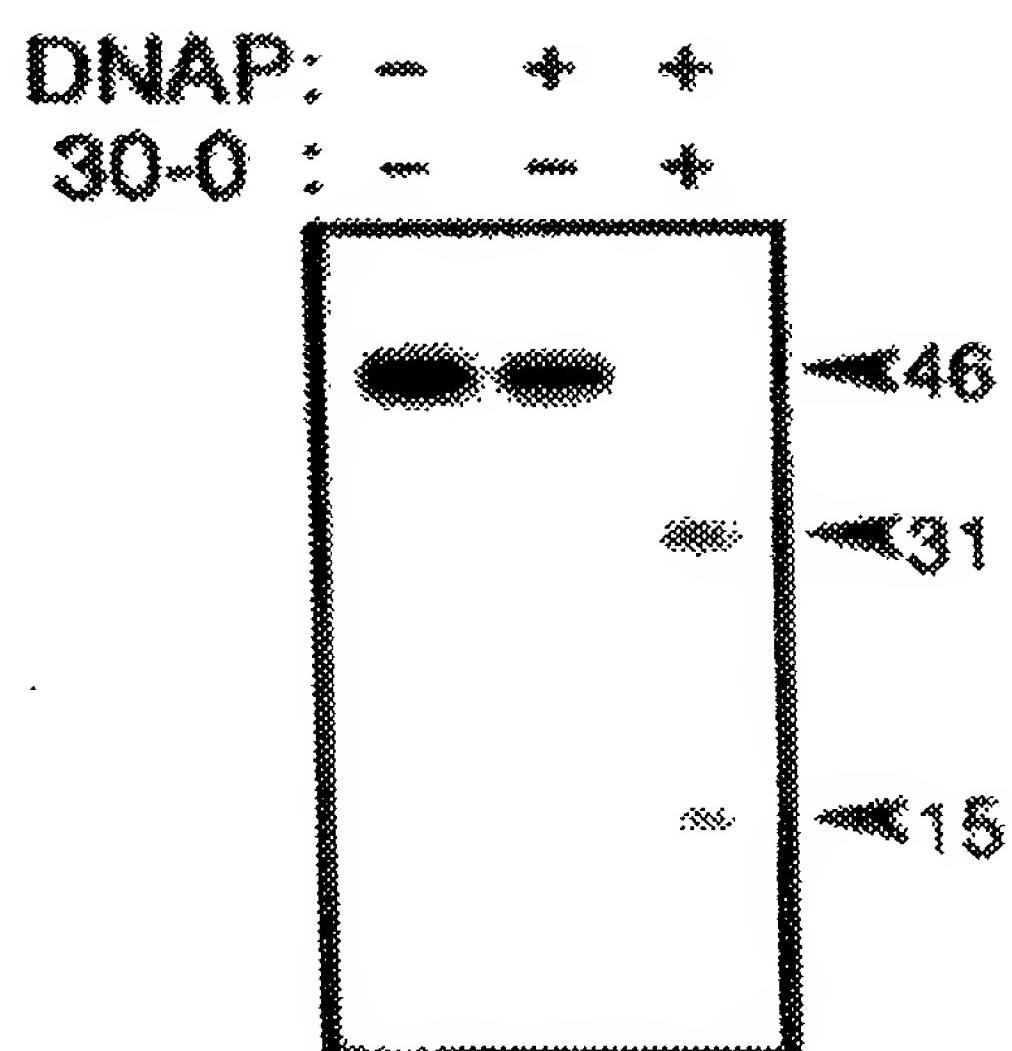
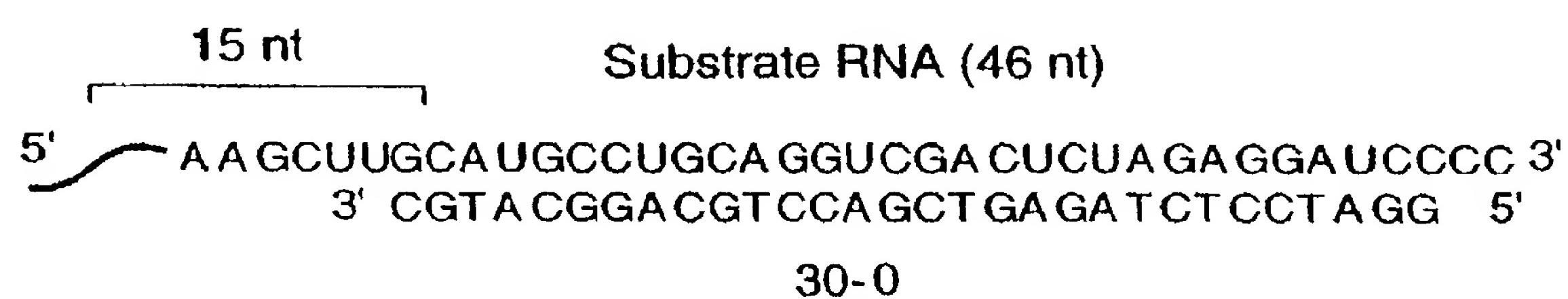


FIG. 13B



5' GATCTTGTGAGGGATAACAATTCACACAGAACAGCG

-35

-10

RBS

TGACAATTATCATCGACTCGTATAATGTTGGATTGAGGGATAACAATTCACACAGAACAGCG
MetAsnSer...
ATGAATTGGAGCTCGGTACCCGGGGATCCTAGAGTCGACCTGCAAGGCATGCAAGCTGGCTGGCC
EcoRI _____ KpnI _____ BamHI _____ Sall _____ XbaI _____ PstI _____ SphI _____
SstI _____

FIG. 14B

FIG. 14A

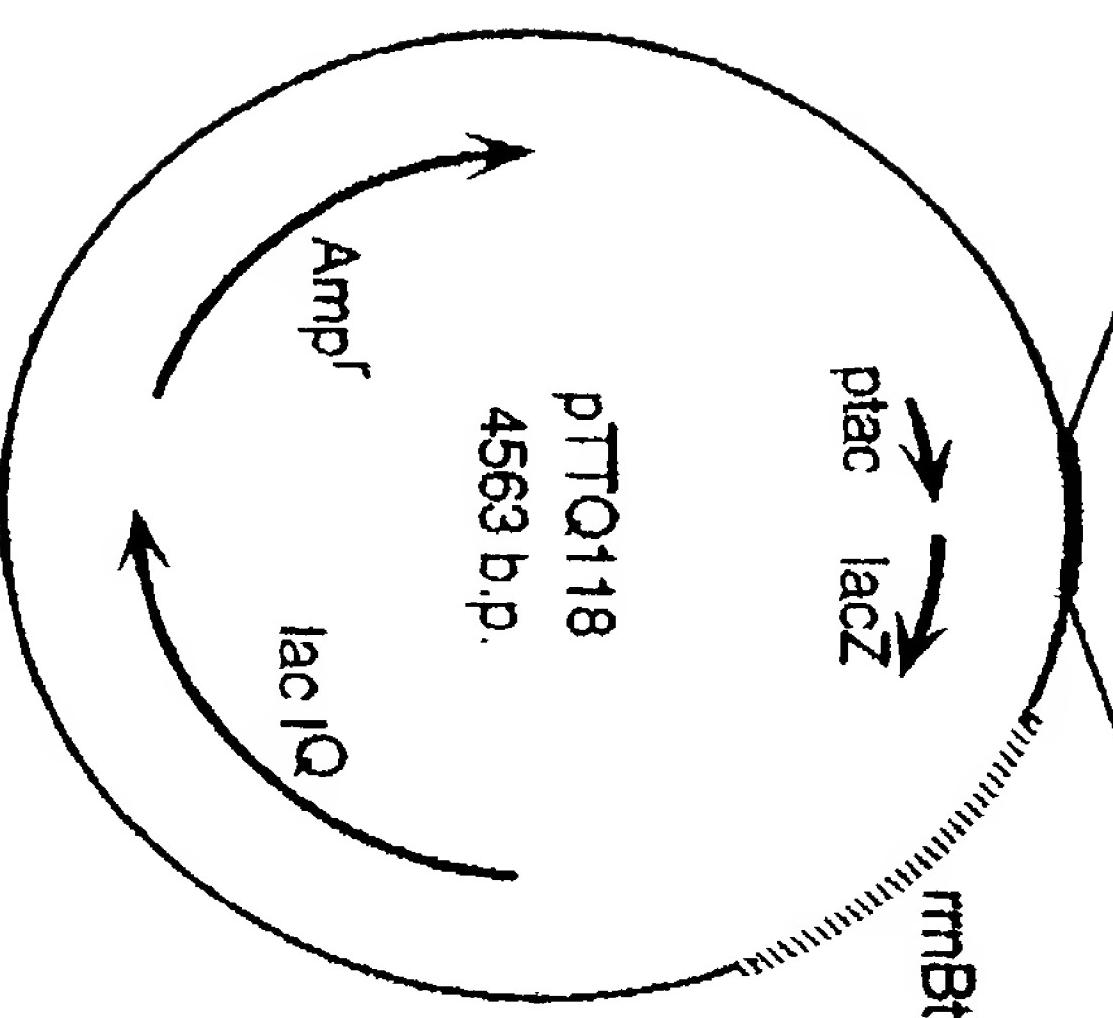


FIG. 14C

RBS: Ribosome binding site
ptac: Synthetic tac promoter
lac IQ: Lac repressor gene

lacZ: Beta-galactosidase alpha fragment
rrnBt: E. coli rrnB transcription terminator

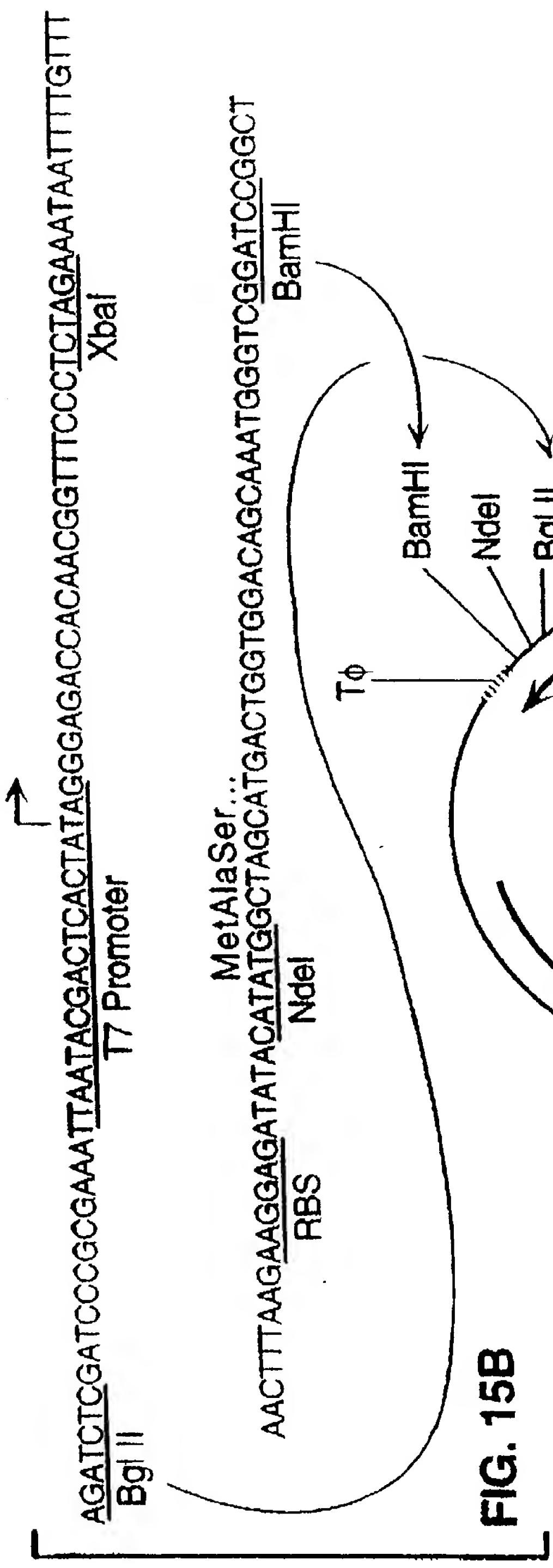


FIG. 15A

RBS: Ribosome binding site

P_{Φ10}: Bacteriophage T7 Φ10 promoter

15C

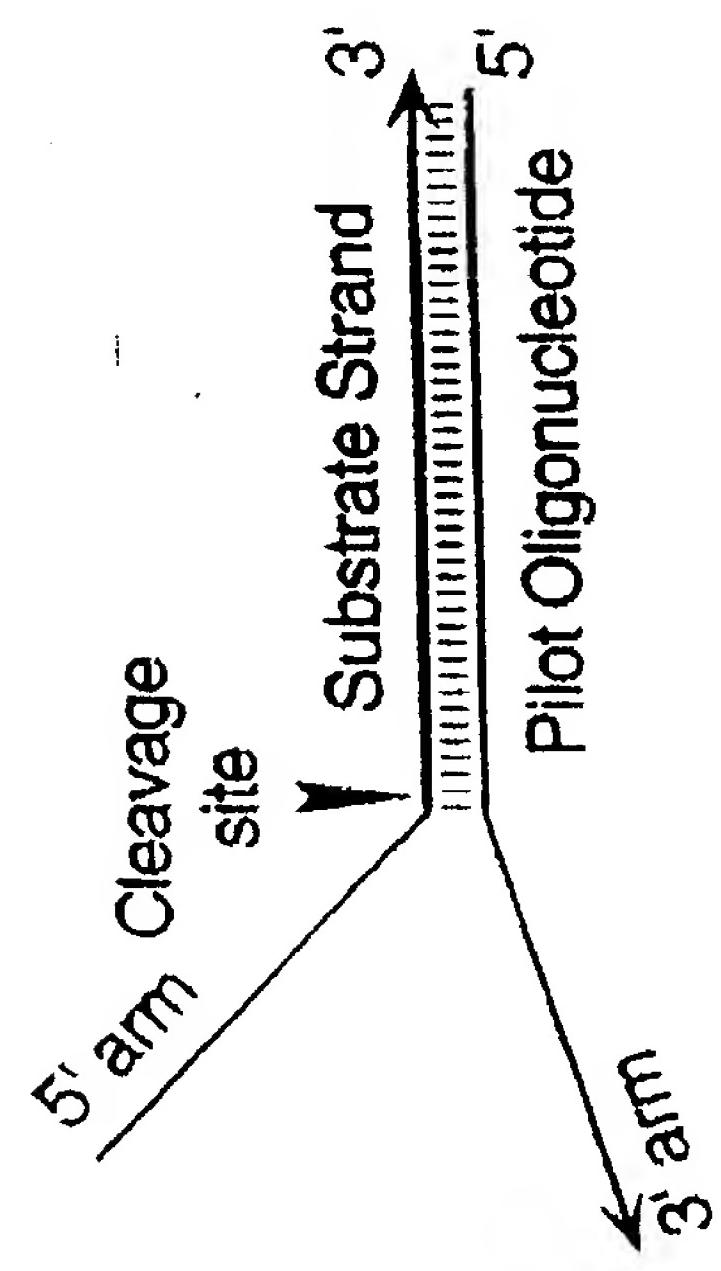


FIG. 16A

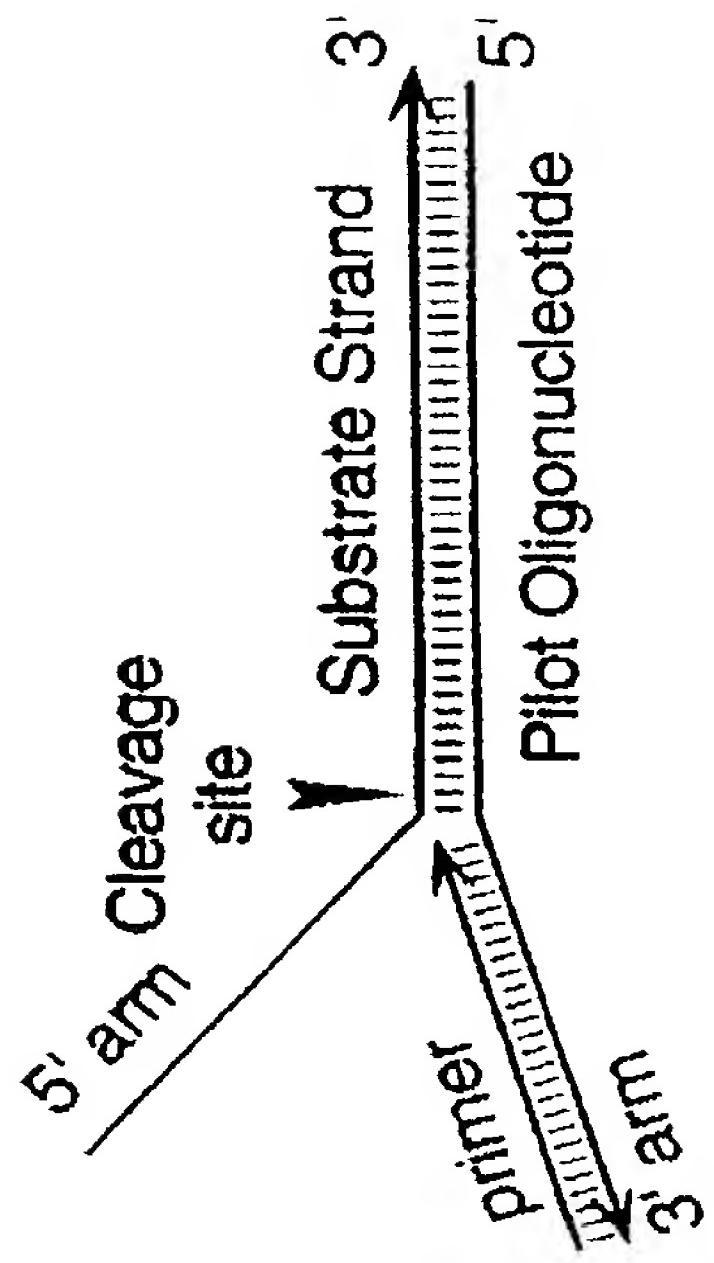


FIG. 16B

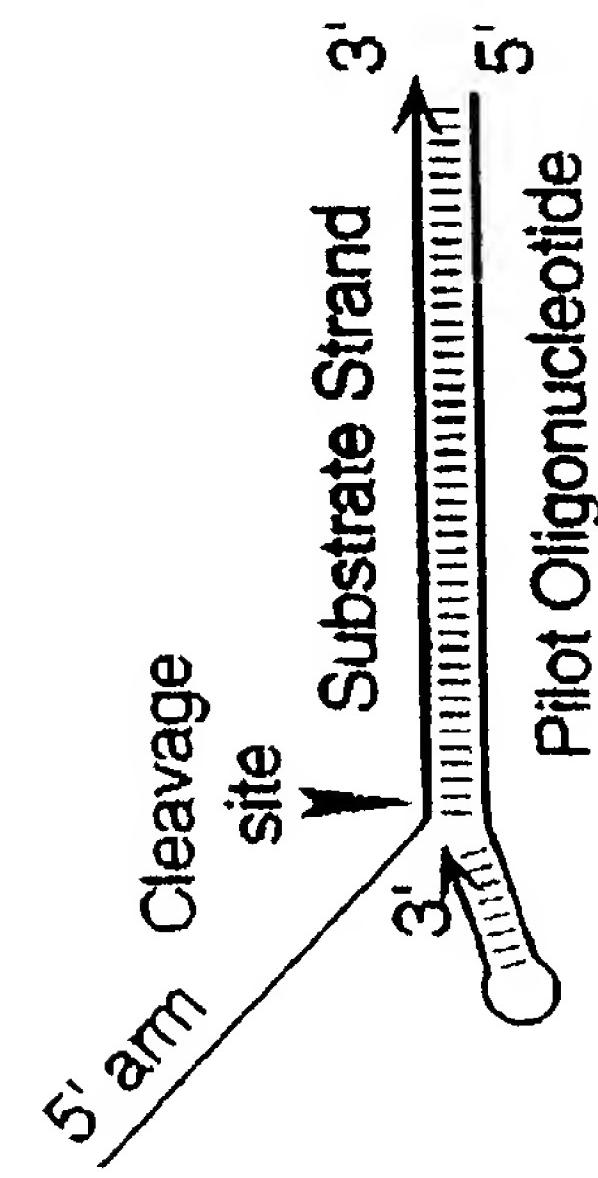


FIG. 16C

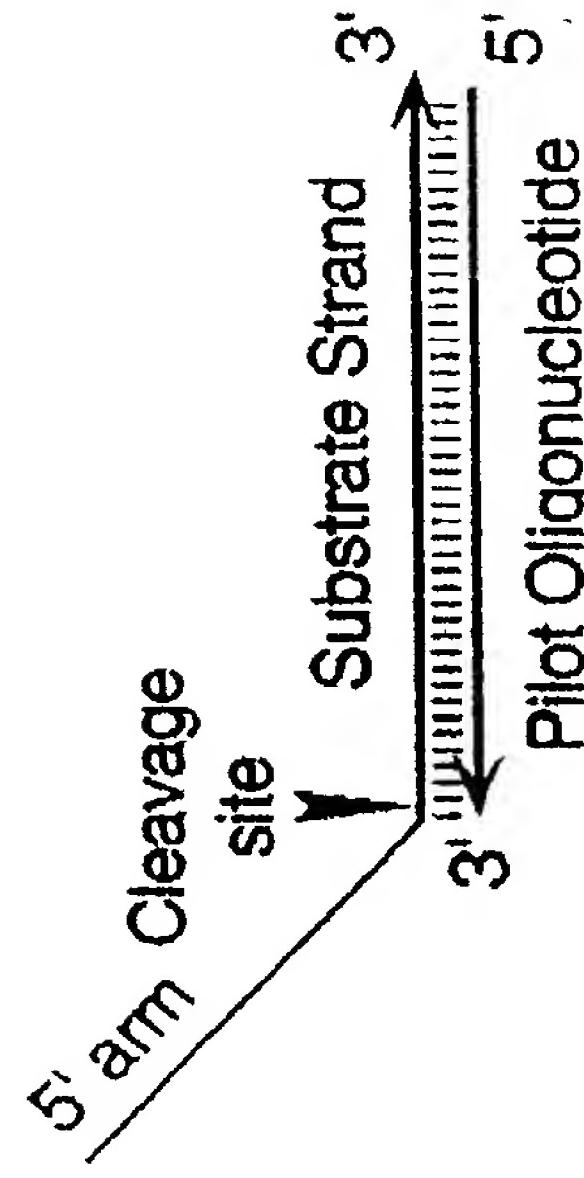


FIG. 16D

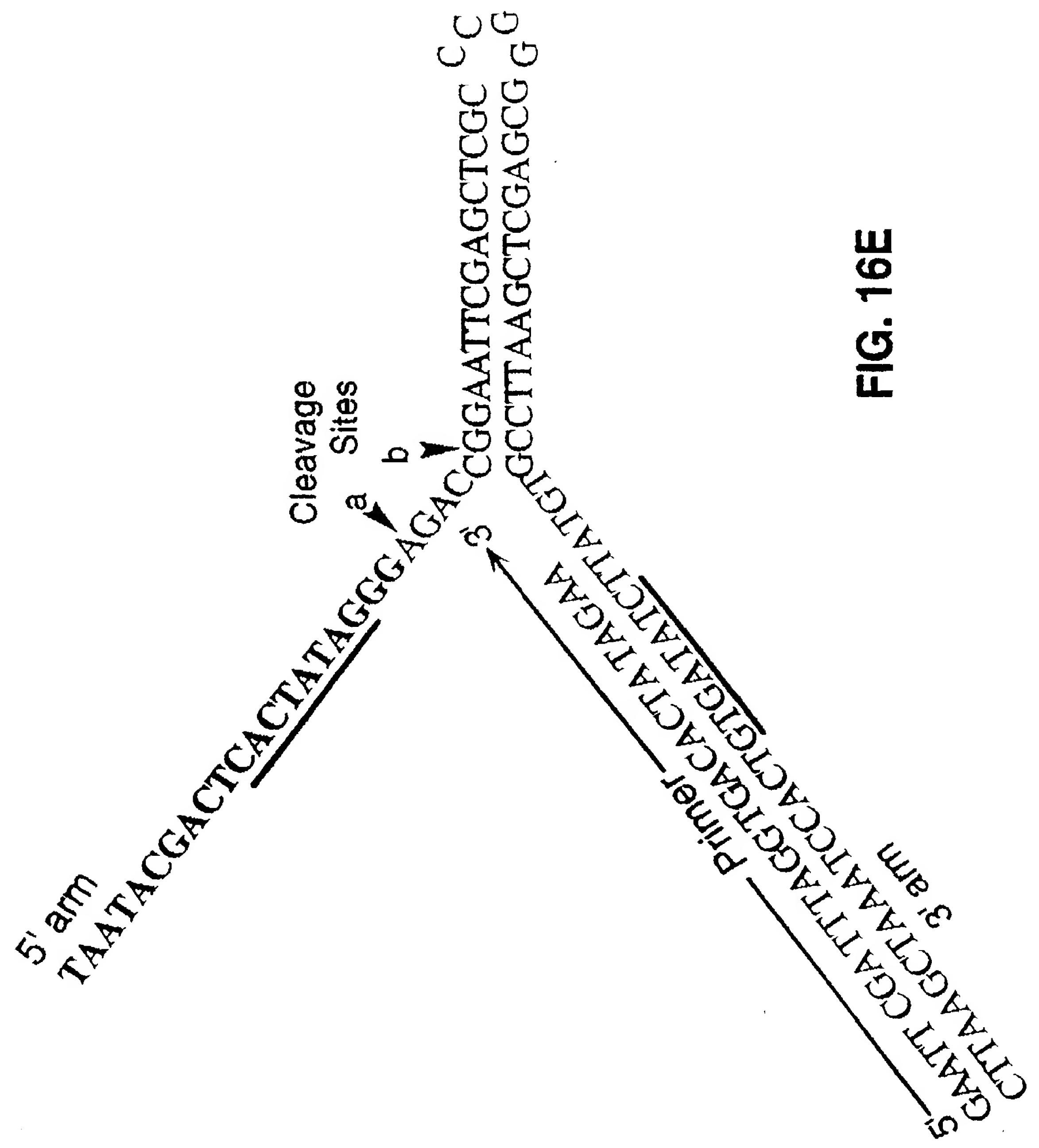


FIG. 16E

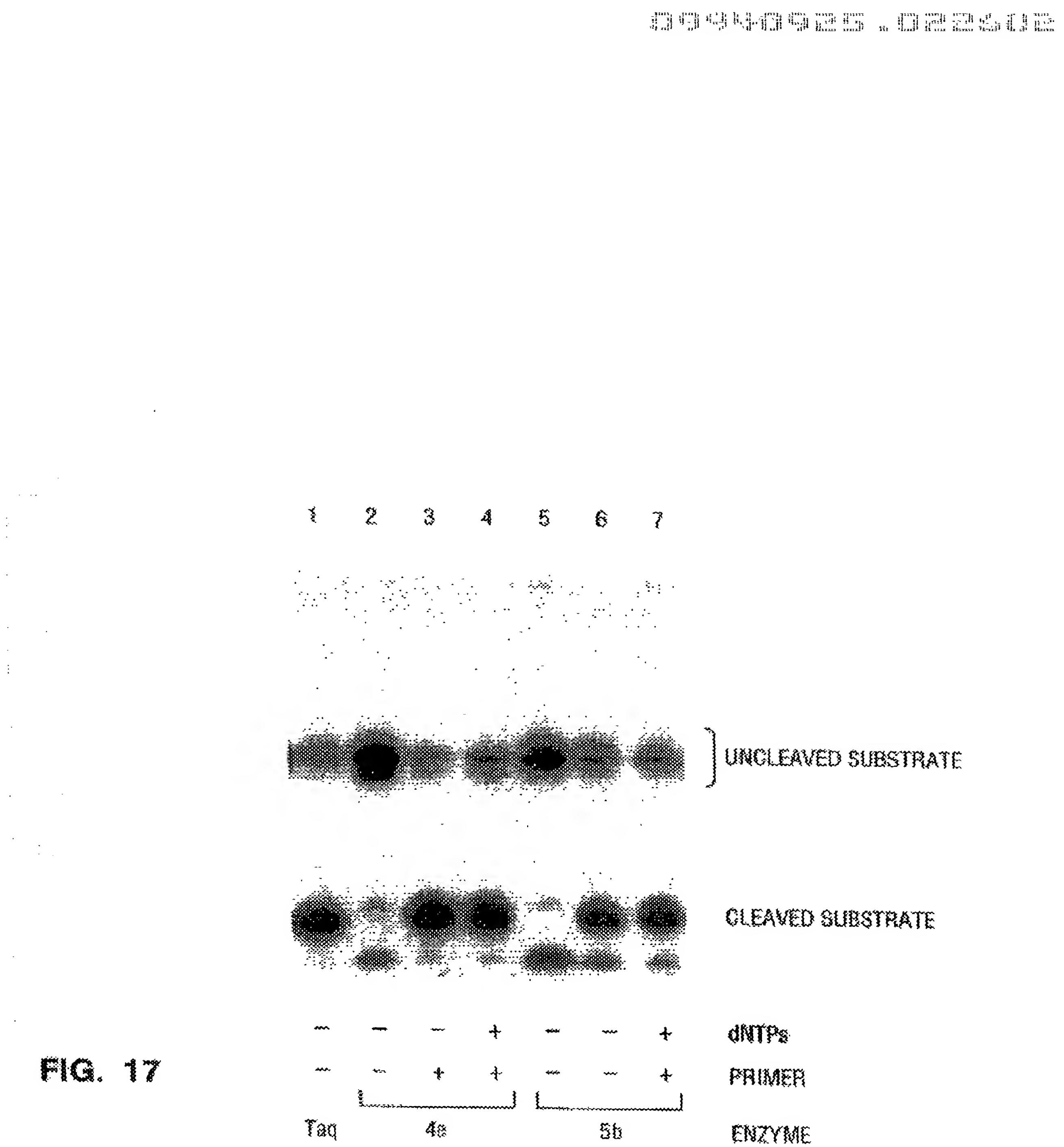


FIG. 17

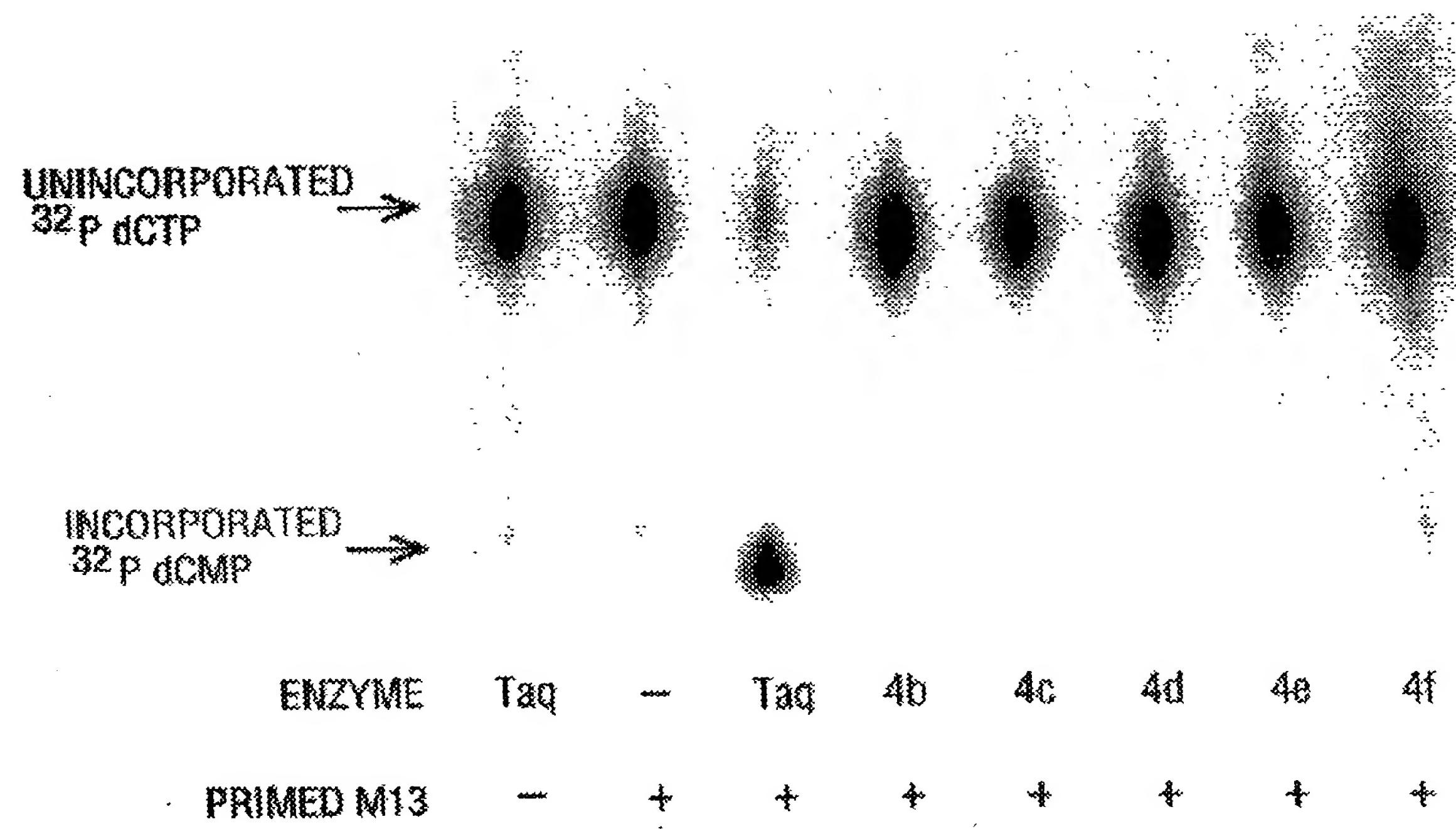


FIG. 18

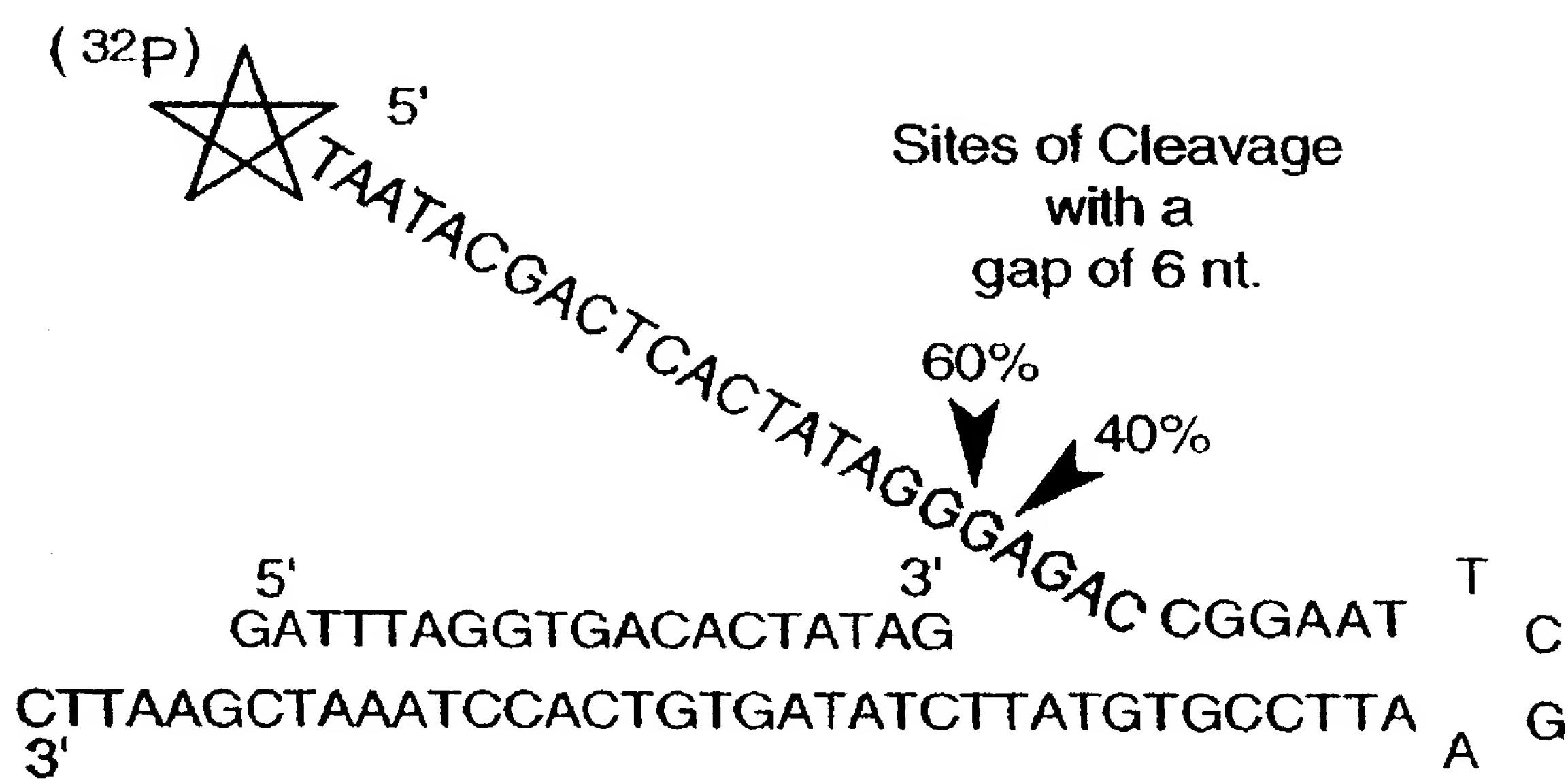


FIG. 19A

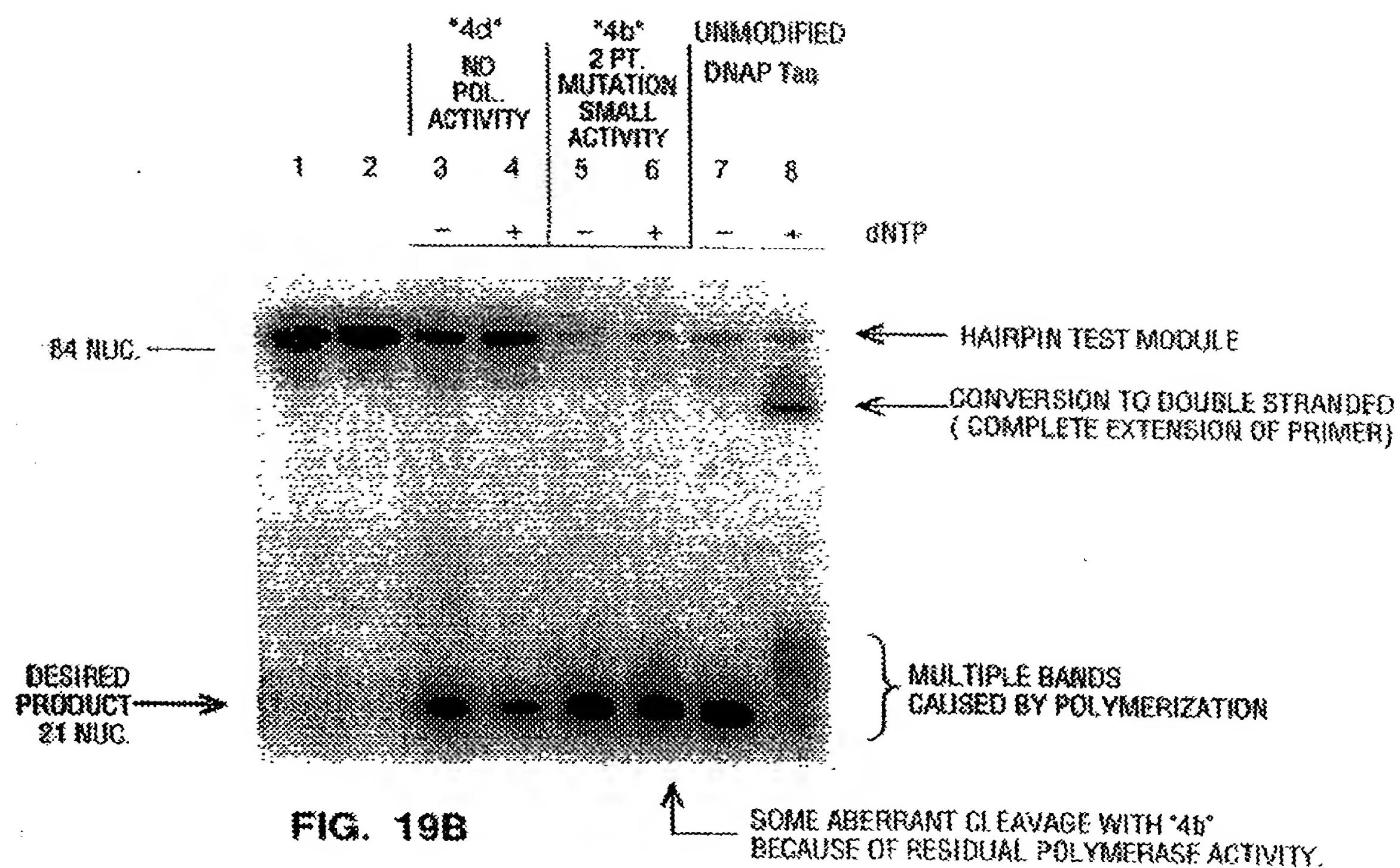
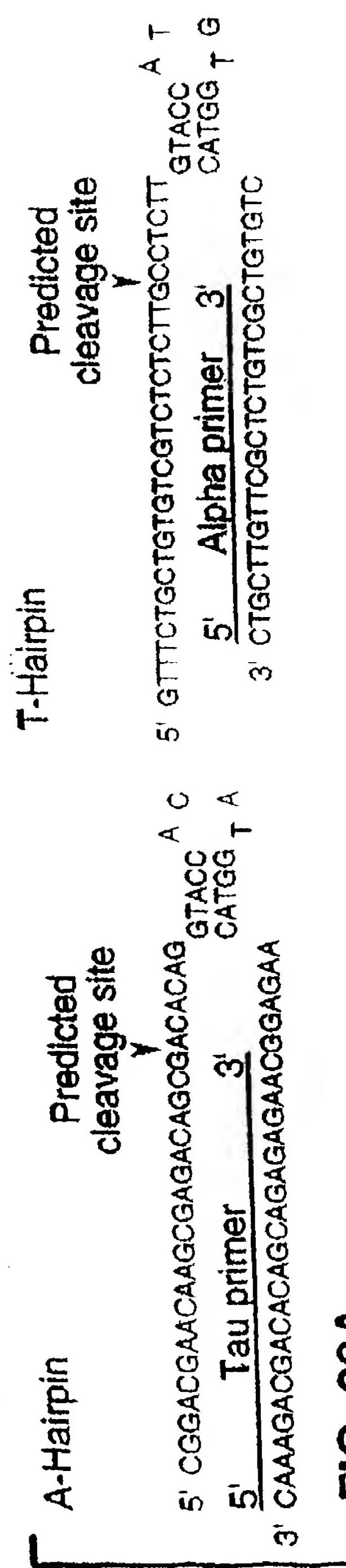


FIG. 19B



Sequence of alpha primer:
 5' GACGAACAAAGCGAGACAGCG 3'

FIG. 20B

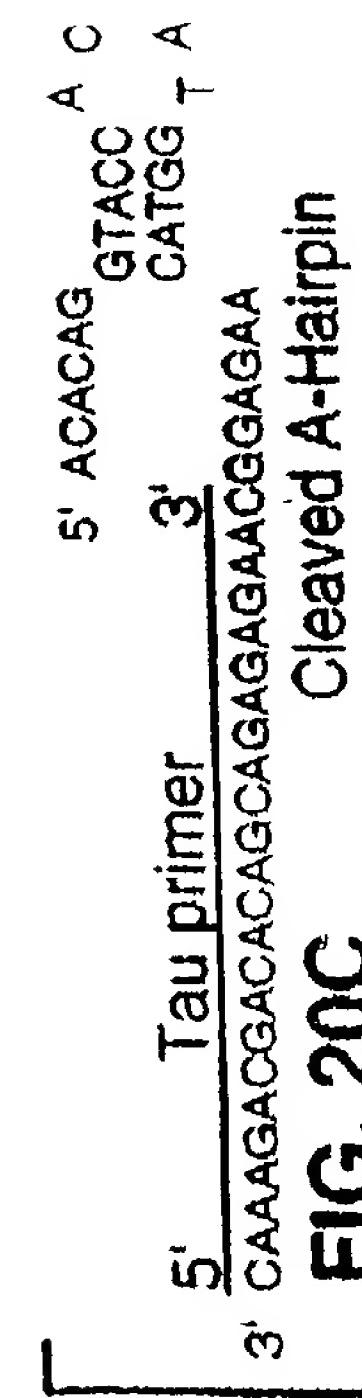
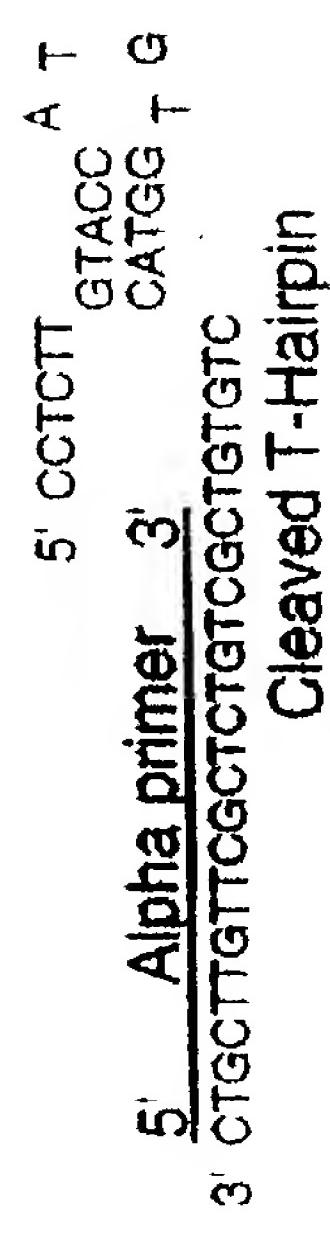


FIG. 20C



NlaIII HgiCI
 MspI RsaI/NlaIV
 RsaI KpnI
 BsmAI

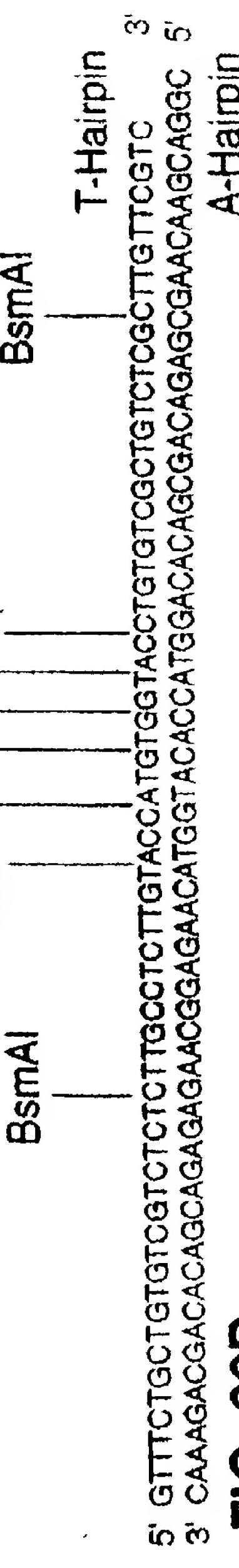
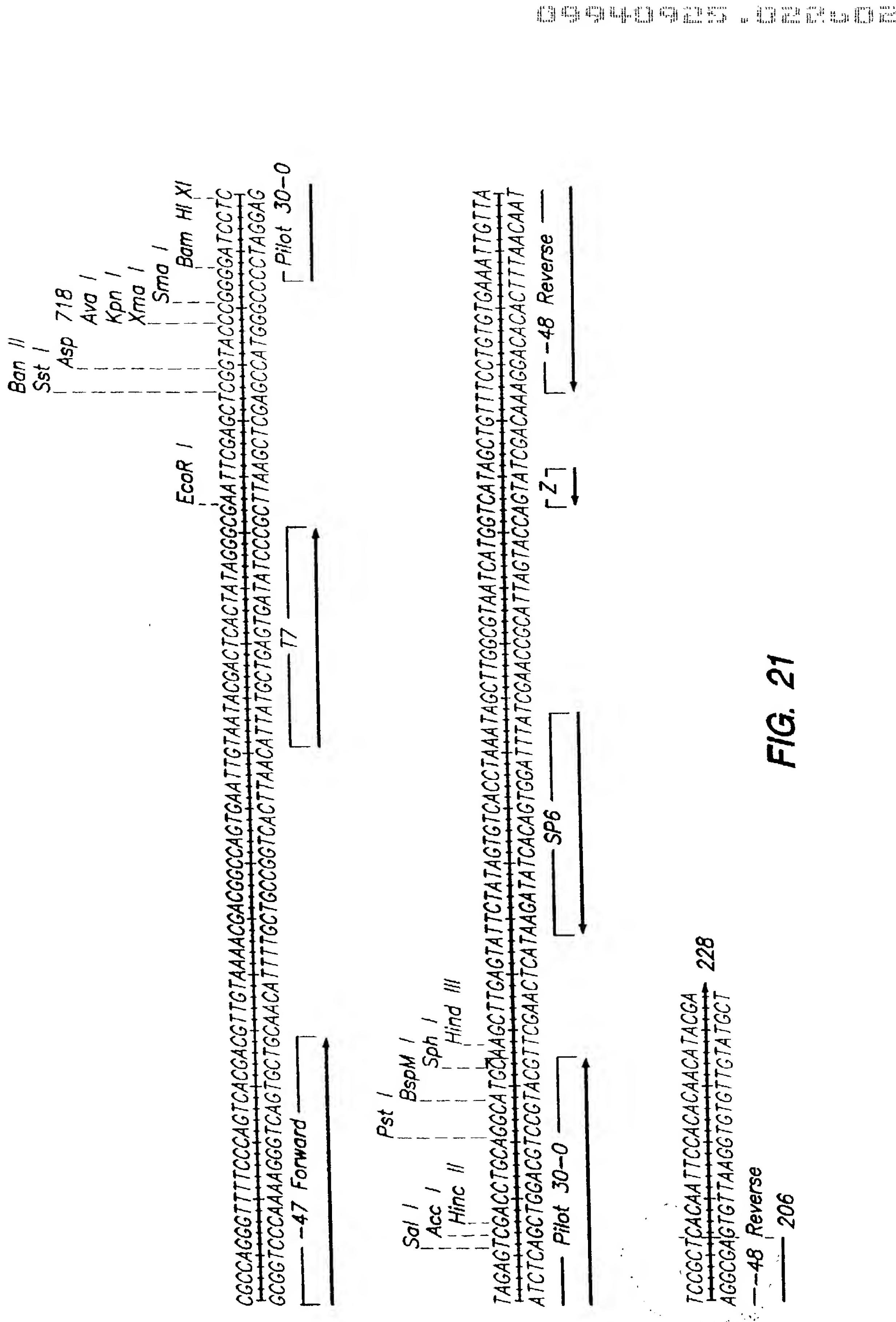


FIG. 20D



EIG 21

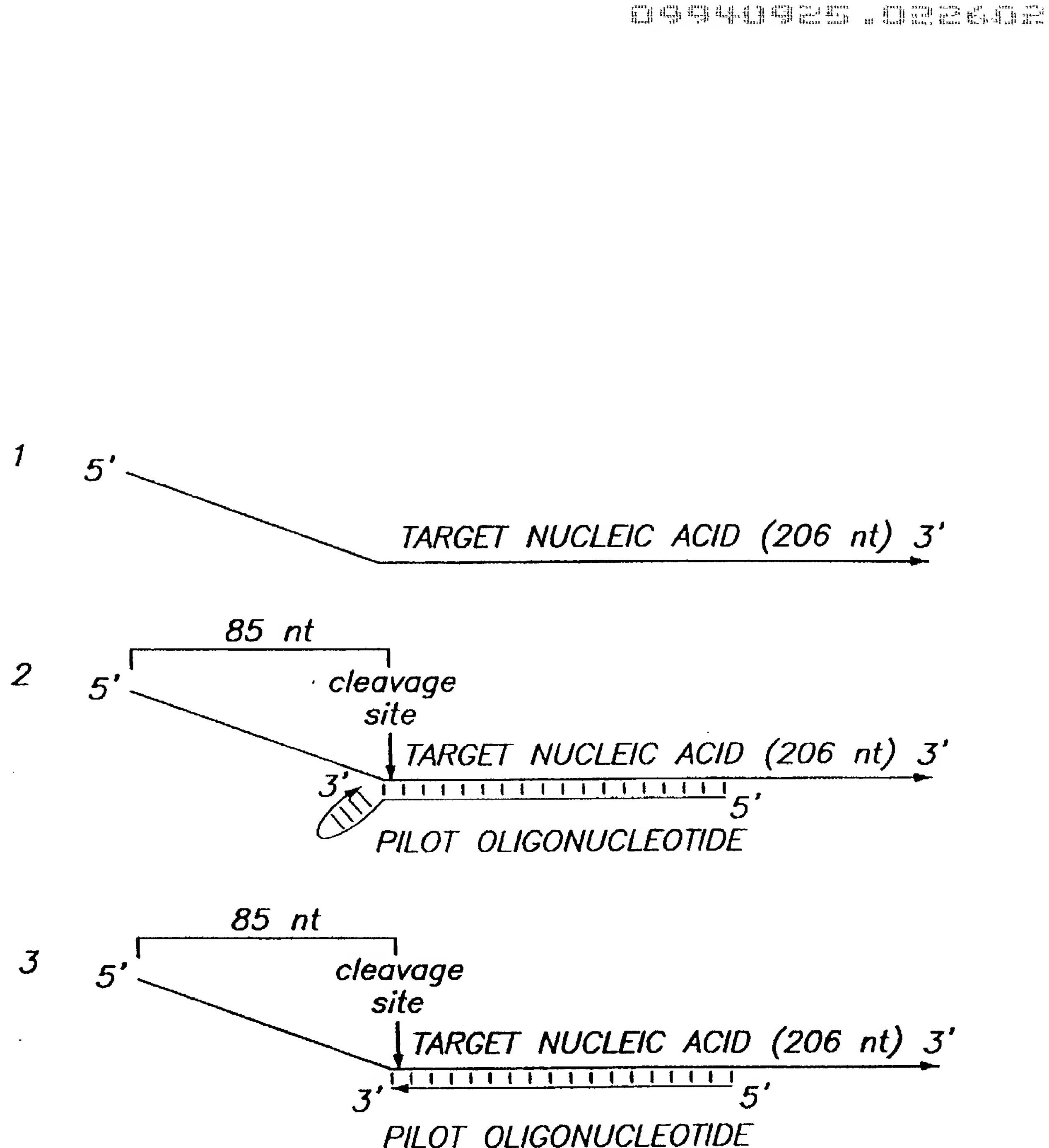


FIG. 22A

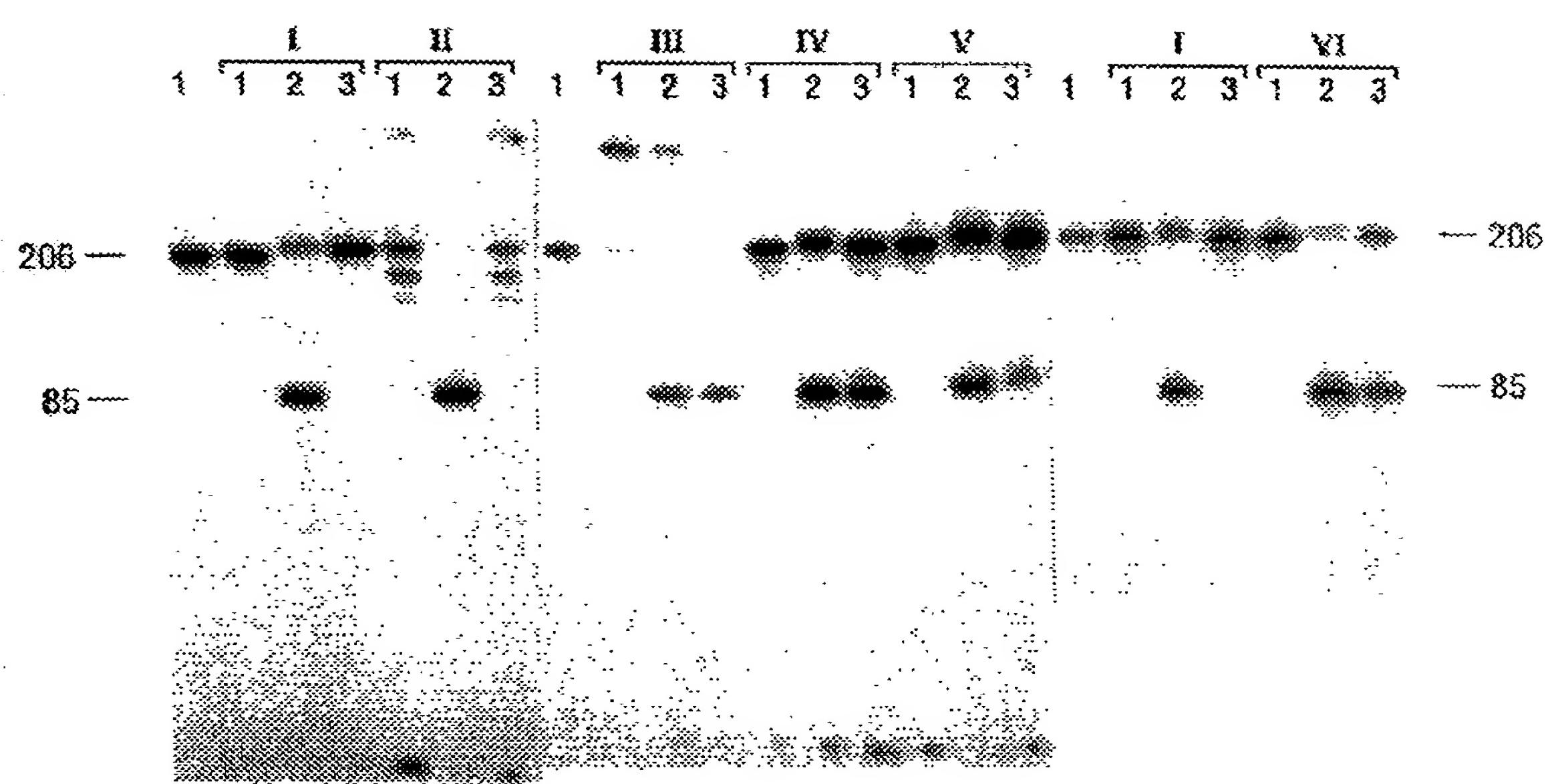


FIG. 22B

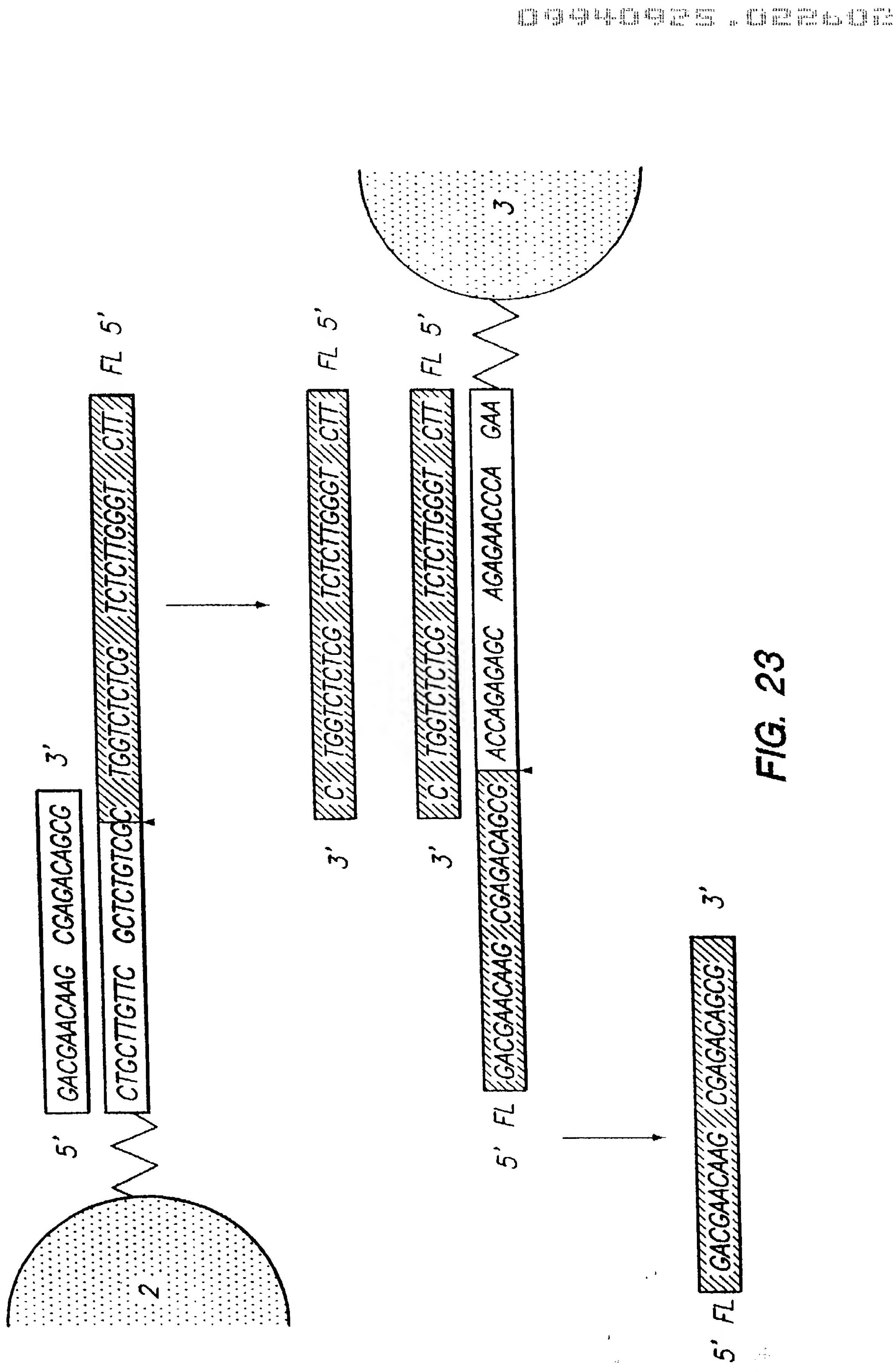


FIG. 23

A T T A T A T A A A

CDR BEAD

T T T A T A T A A A

PILOT

- - + - + + - -

CLEAVASE

M M - + + + + + - M M

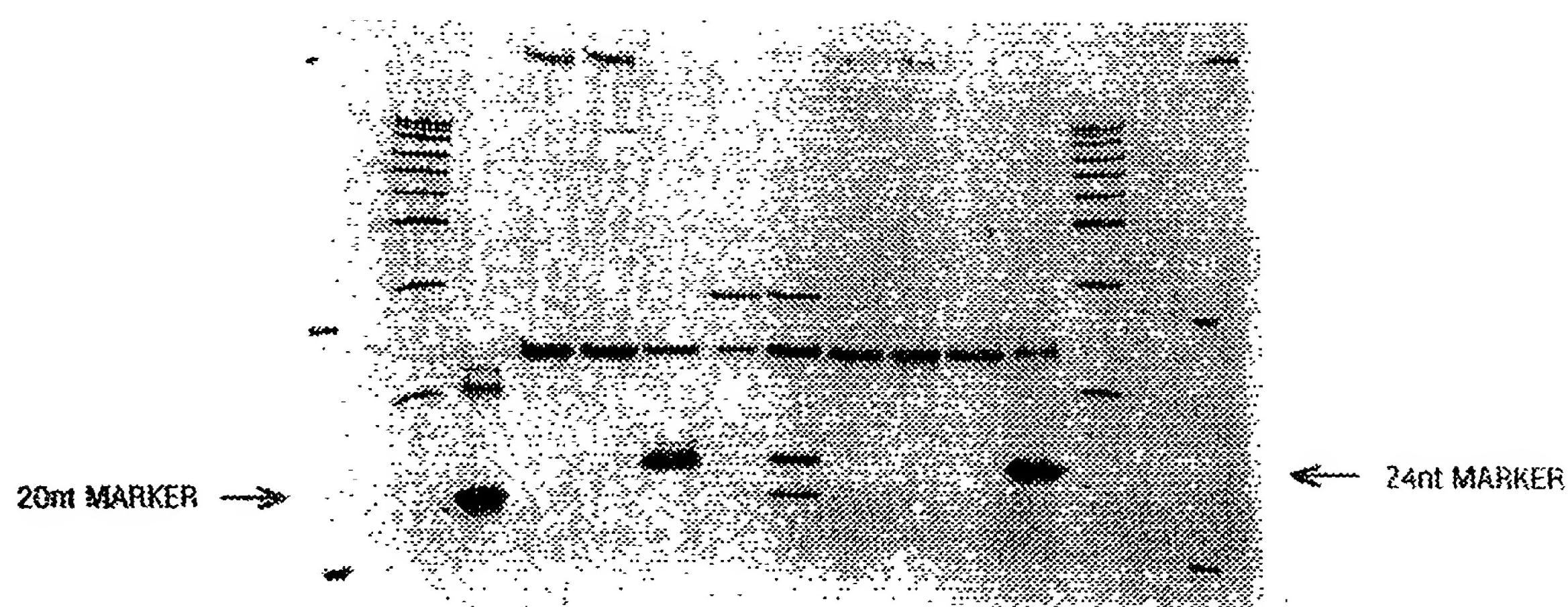


FIG. 24

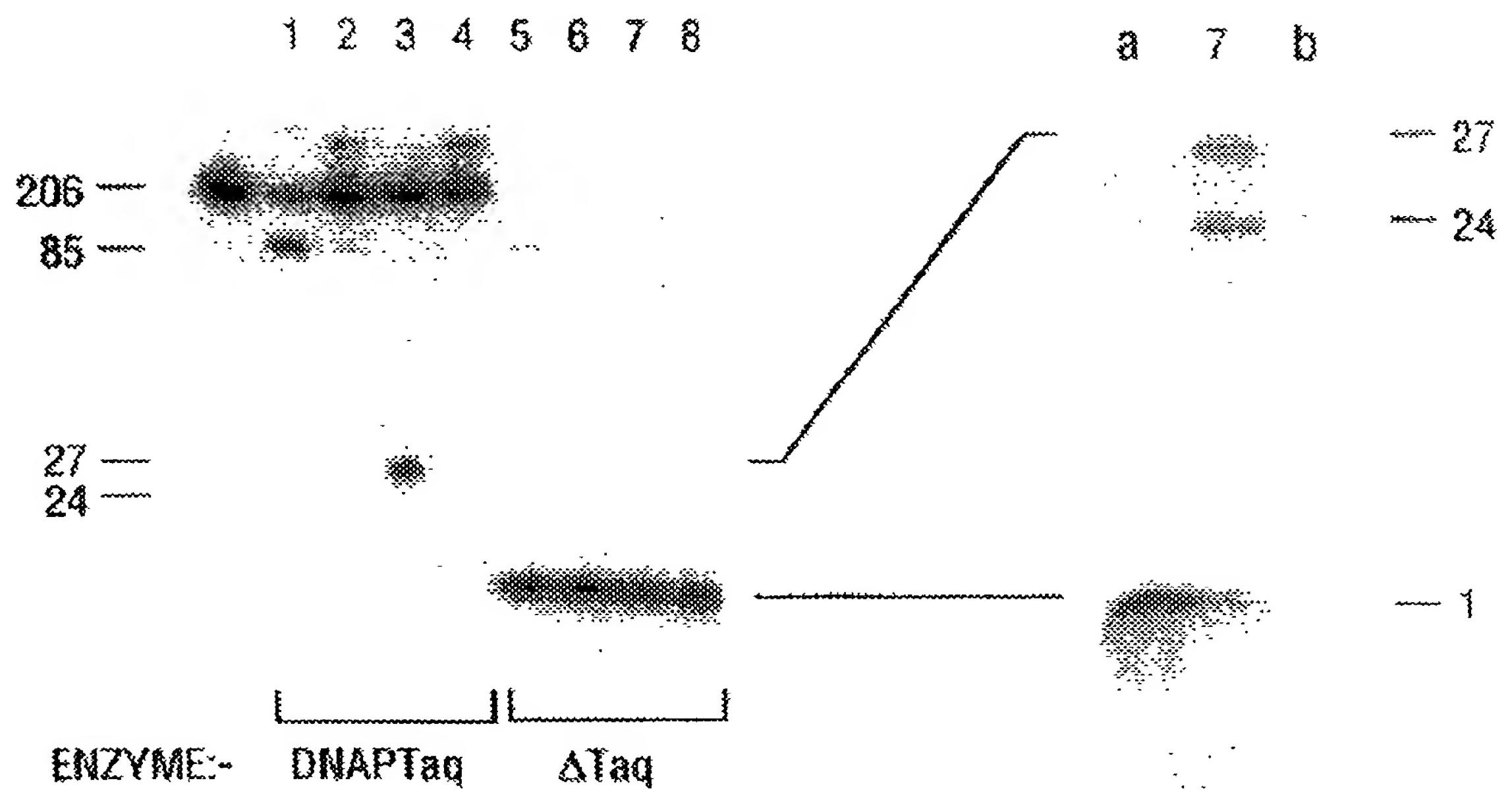


FIG. 25A

FIG. 25B

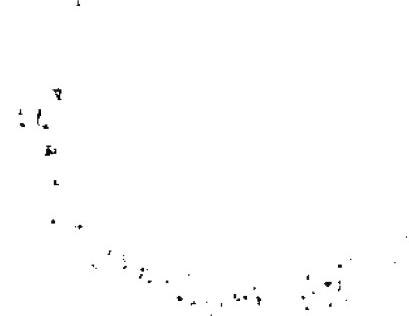


FIG. 26A

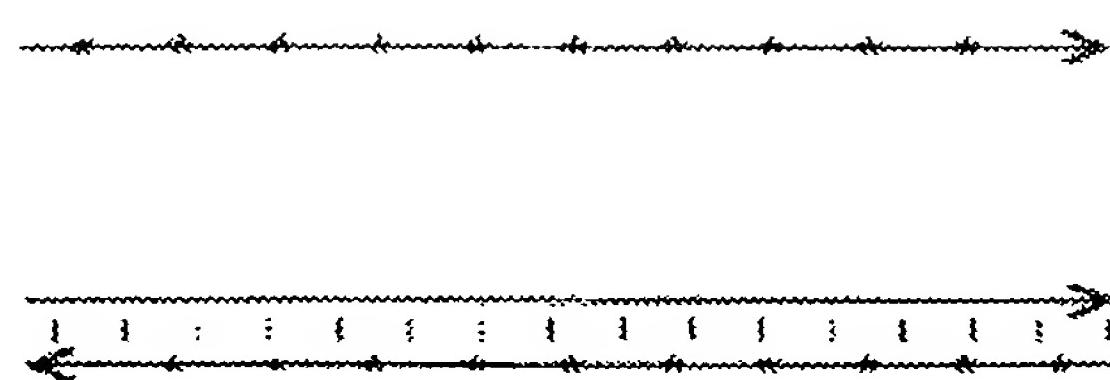
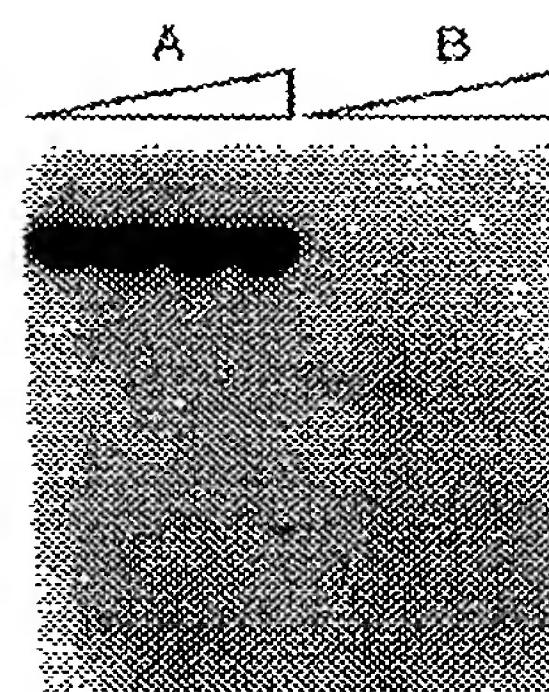


FIG. 26B

* = 32p



— 206

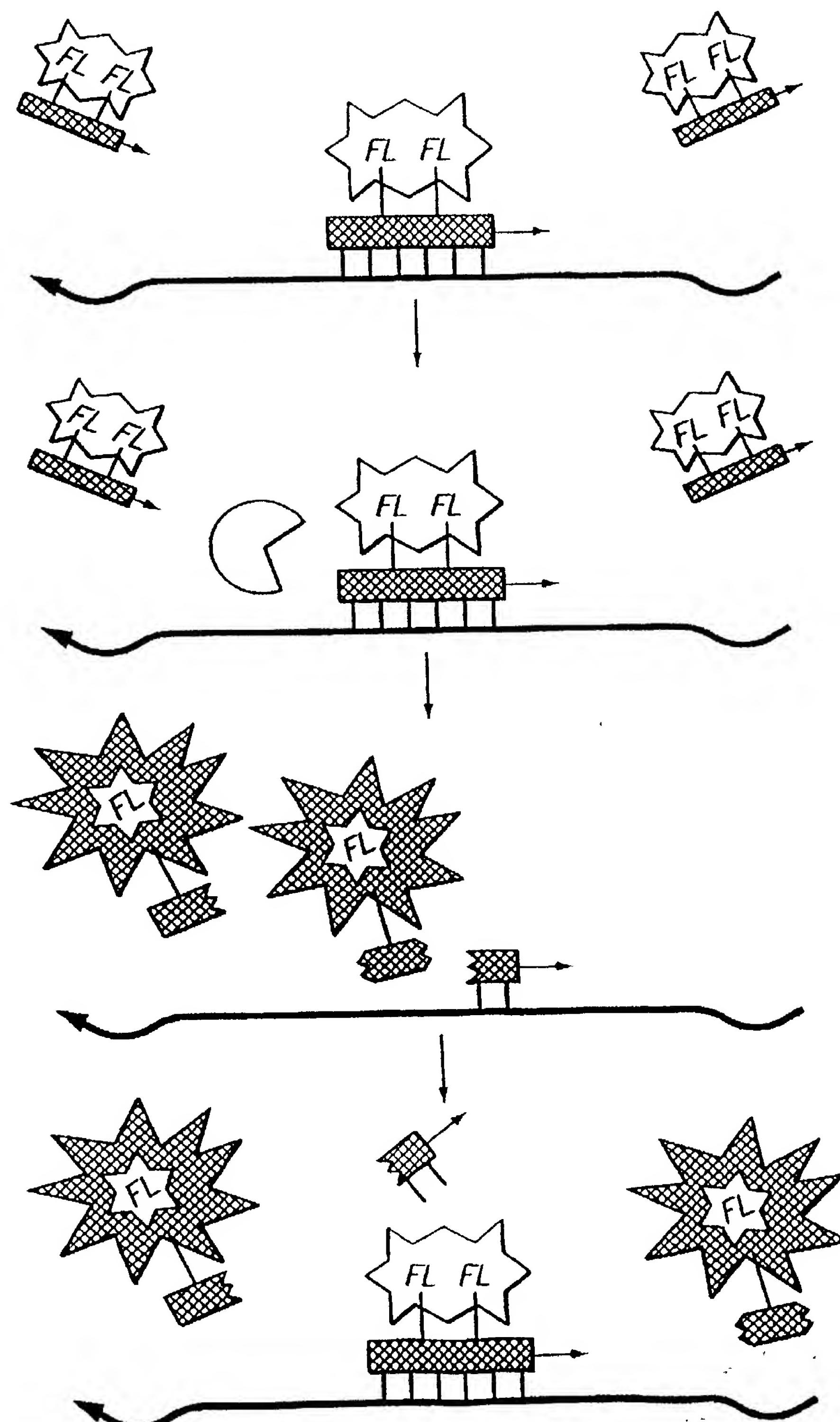


FIG. 27

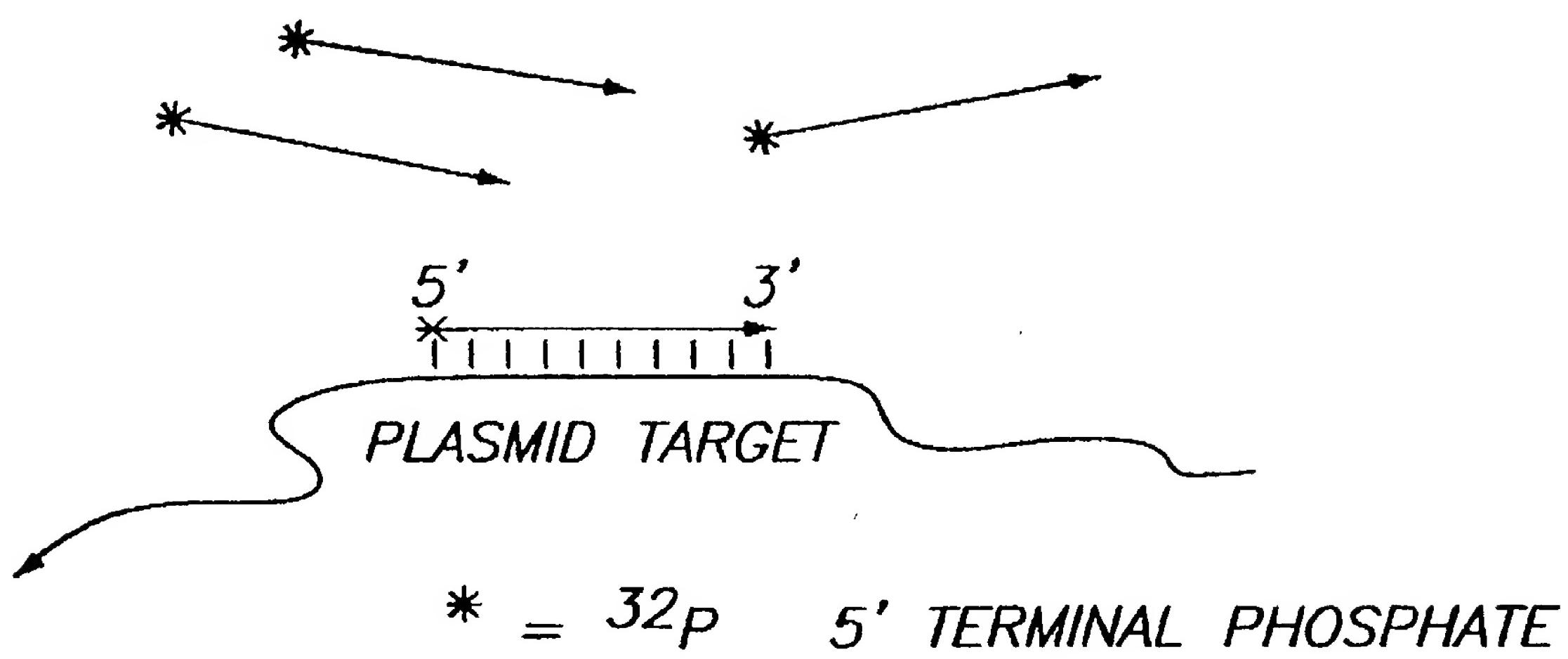


FIG. 28A

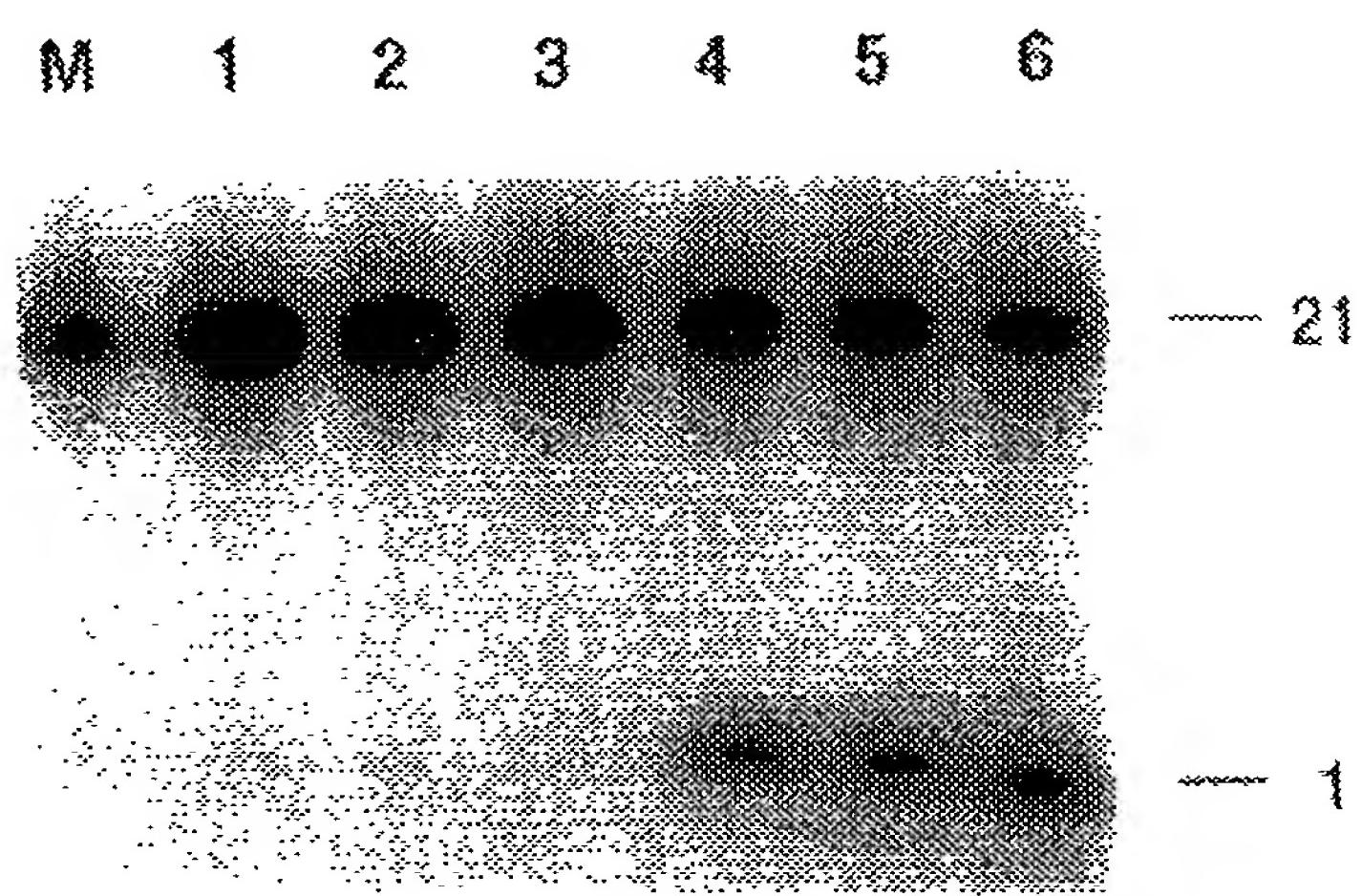


FIG. 28B

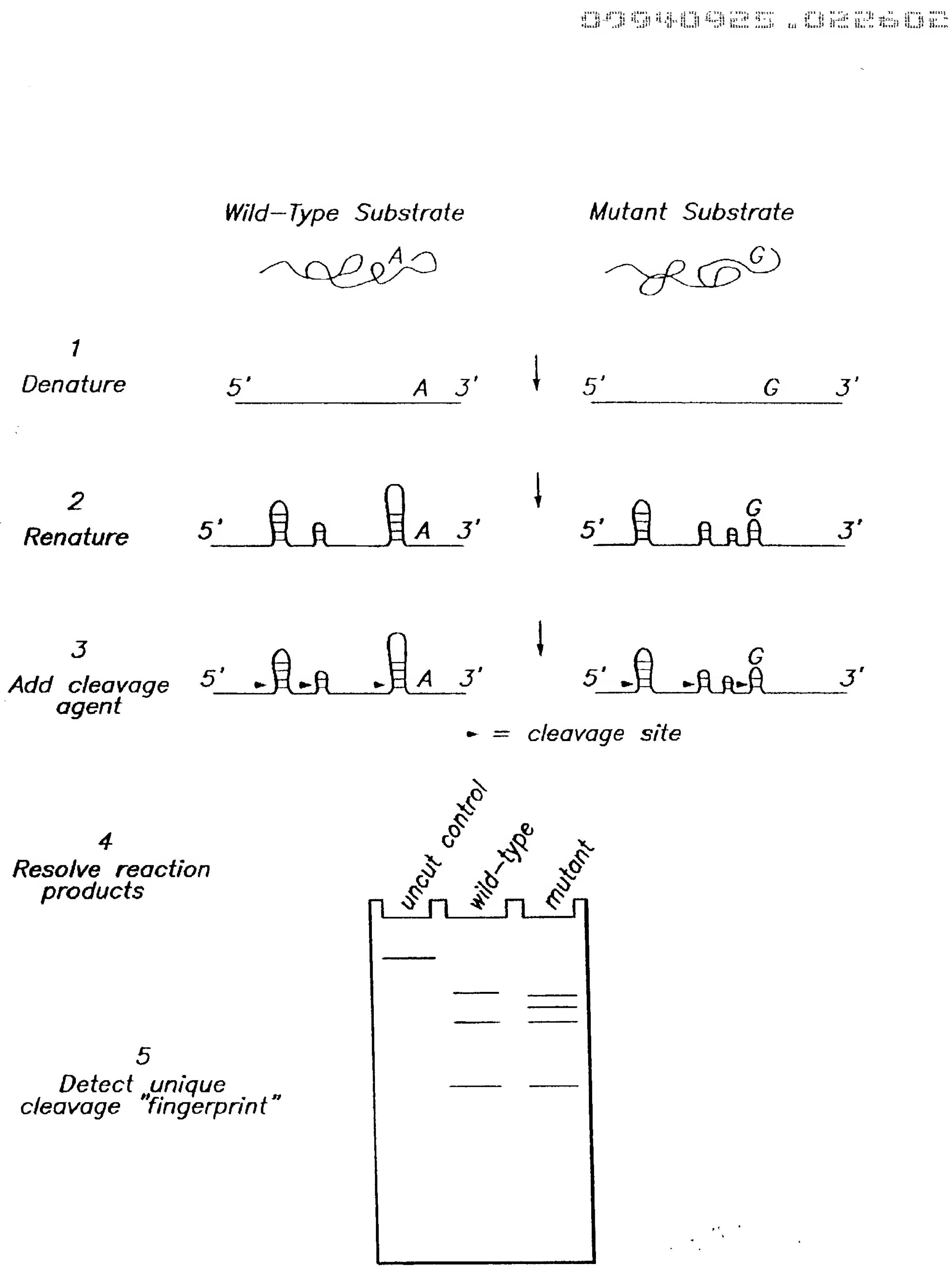


FIG. 29

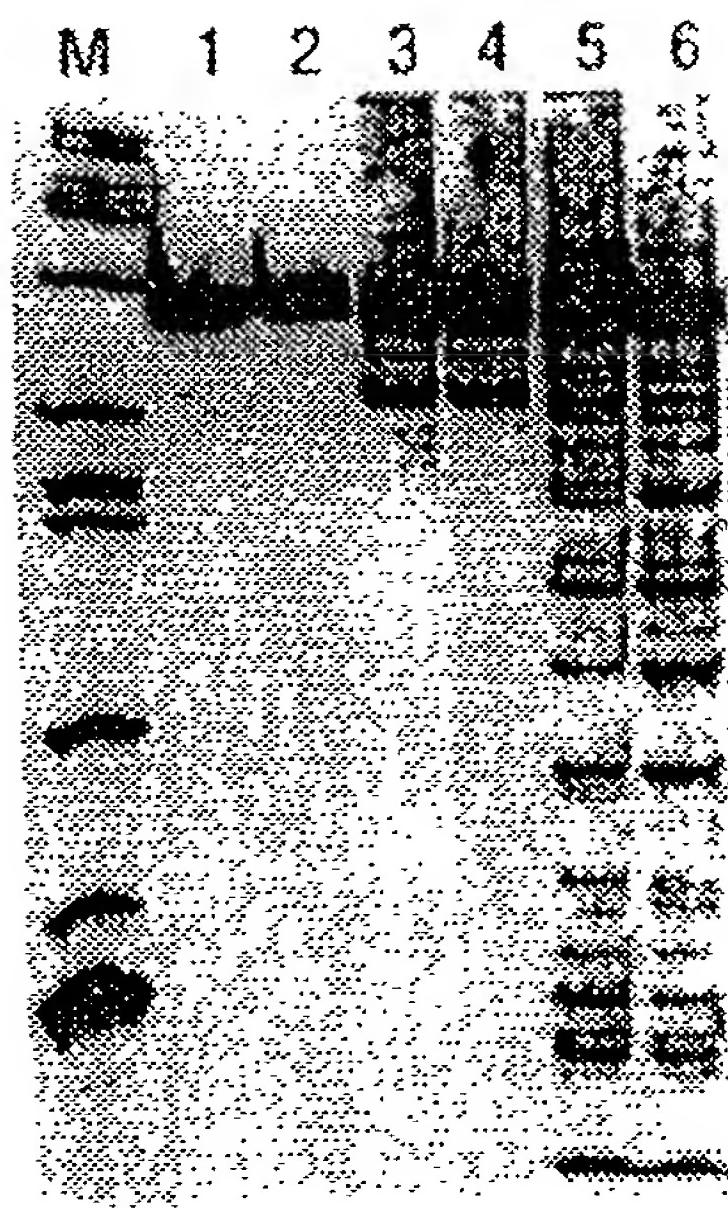


FIG. 30

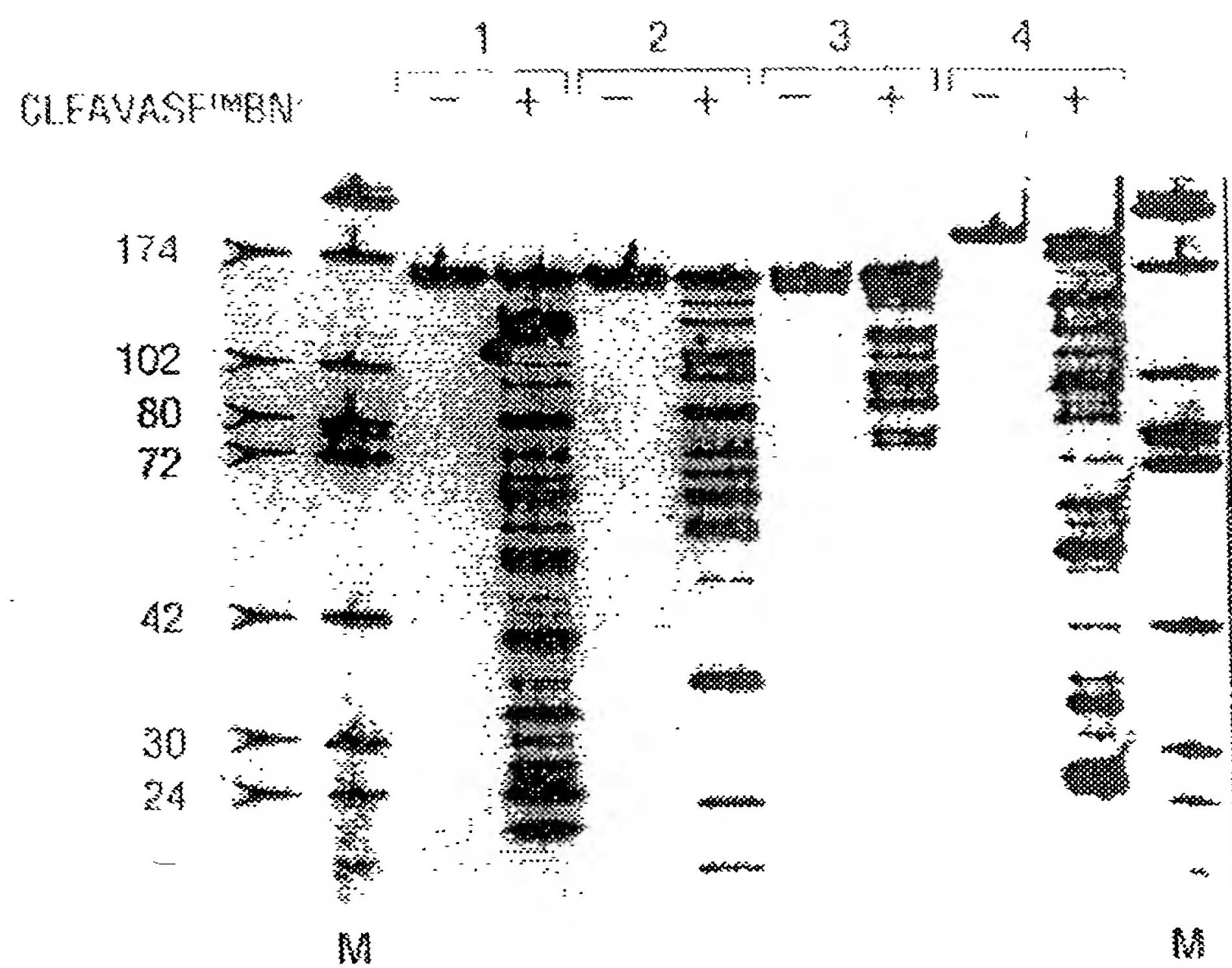


FIG. 31

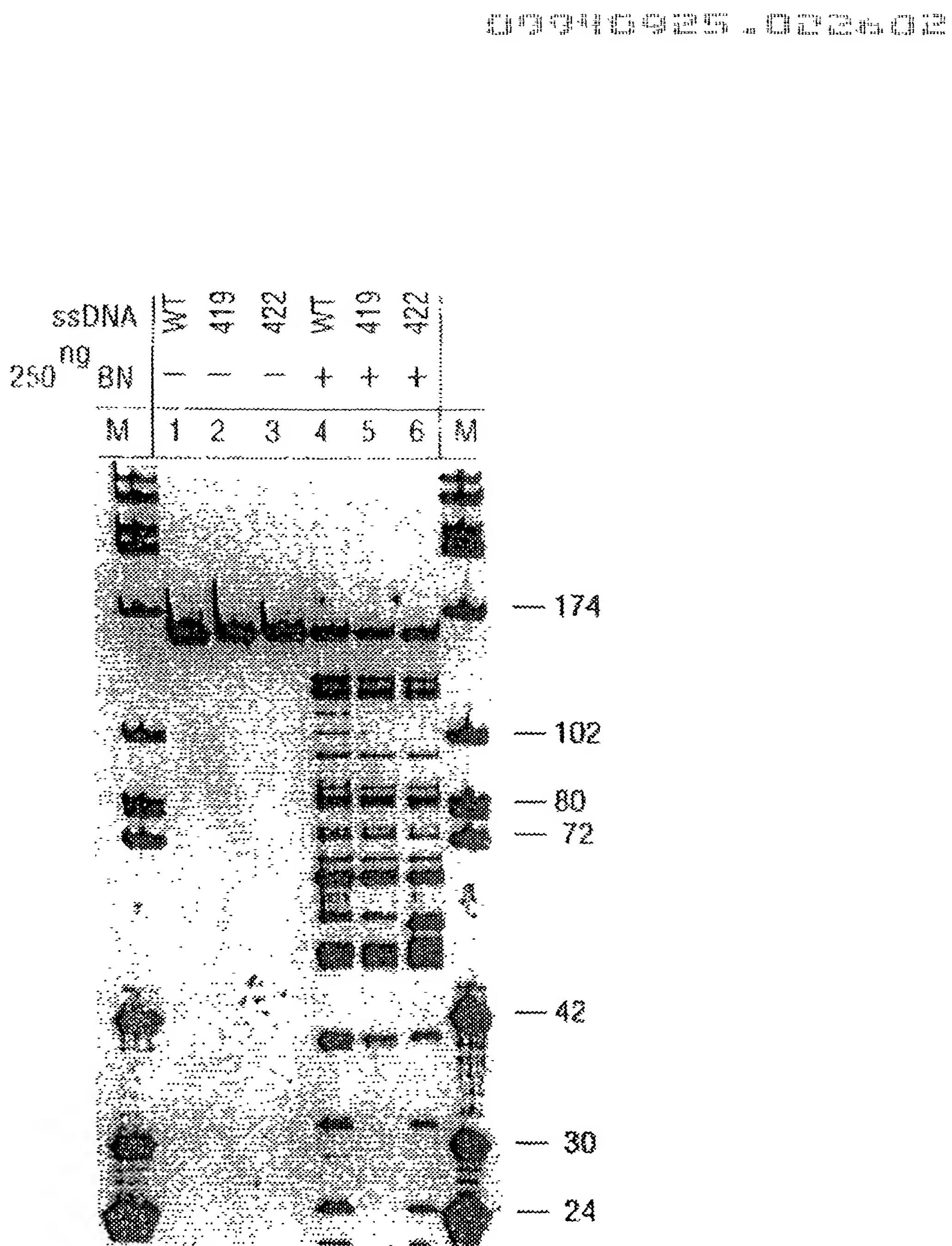
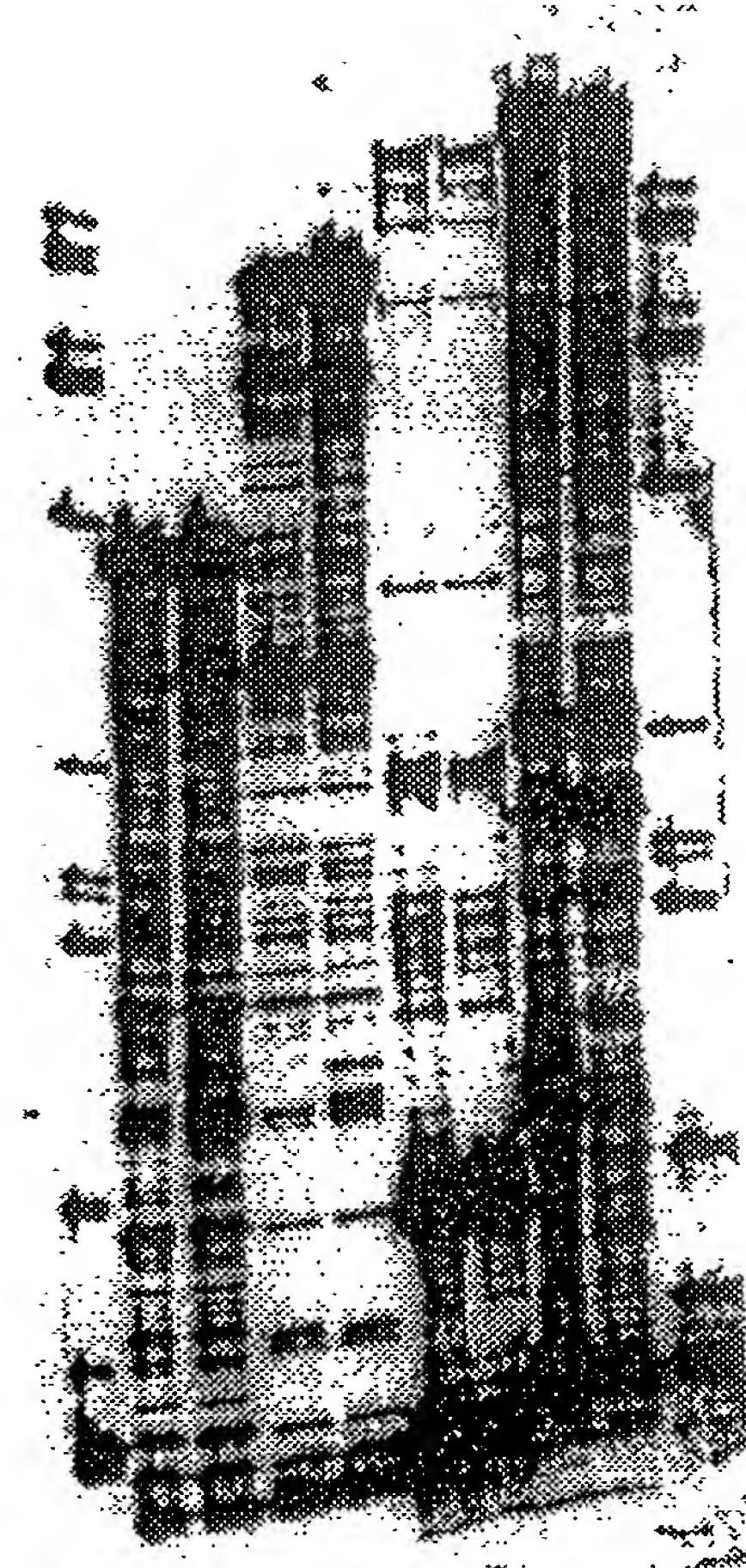


FIG. 32

157 378 1056 1587
M 1 2 3 4 5 6 7 8 M



WT 422 WT 422 WT 422 WT 422

FIG. 33

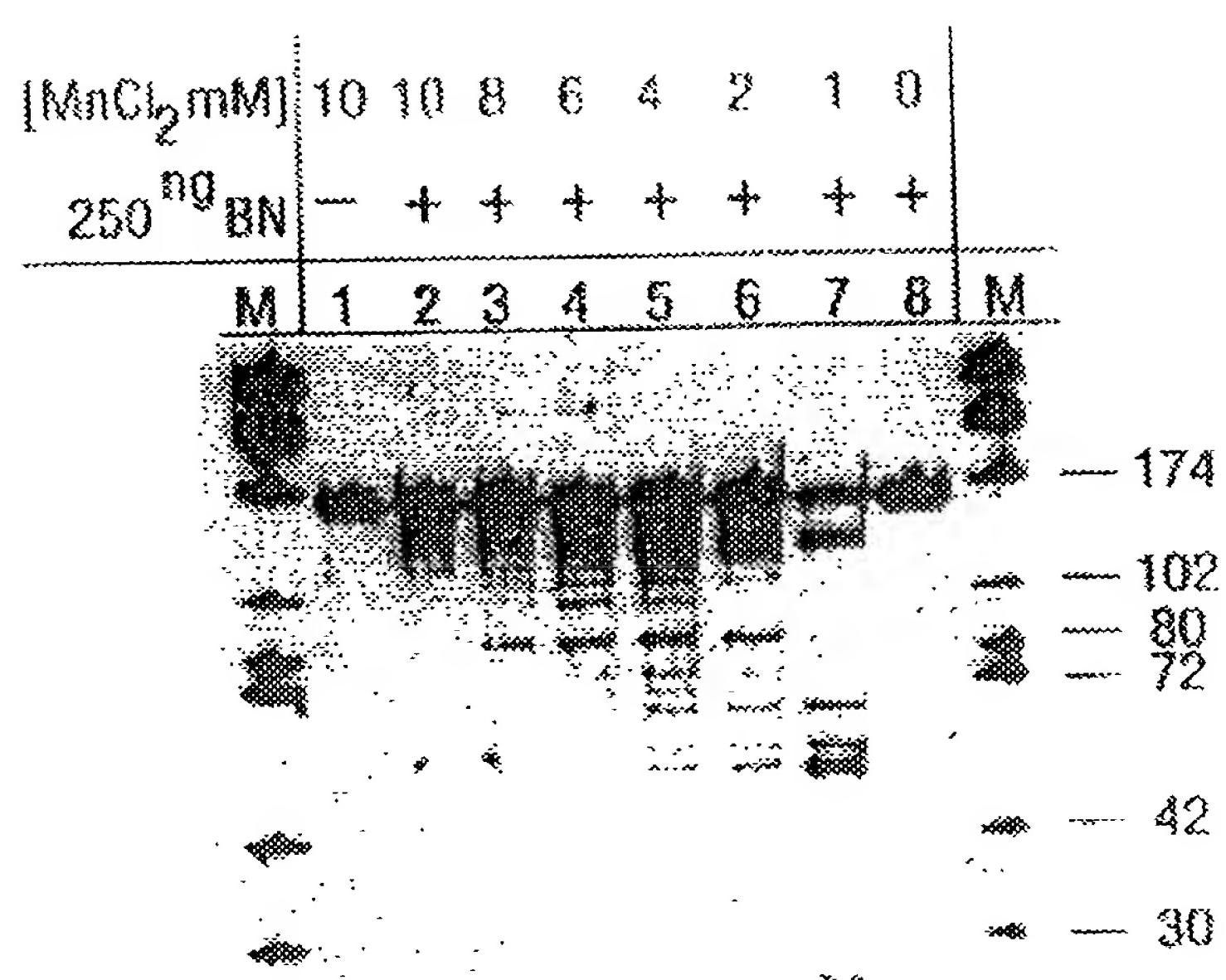


FIG. 34

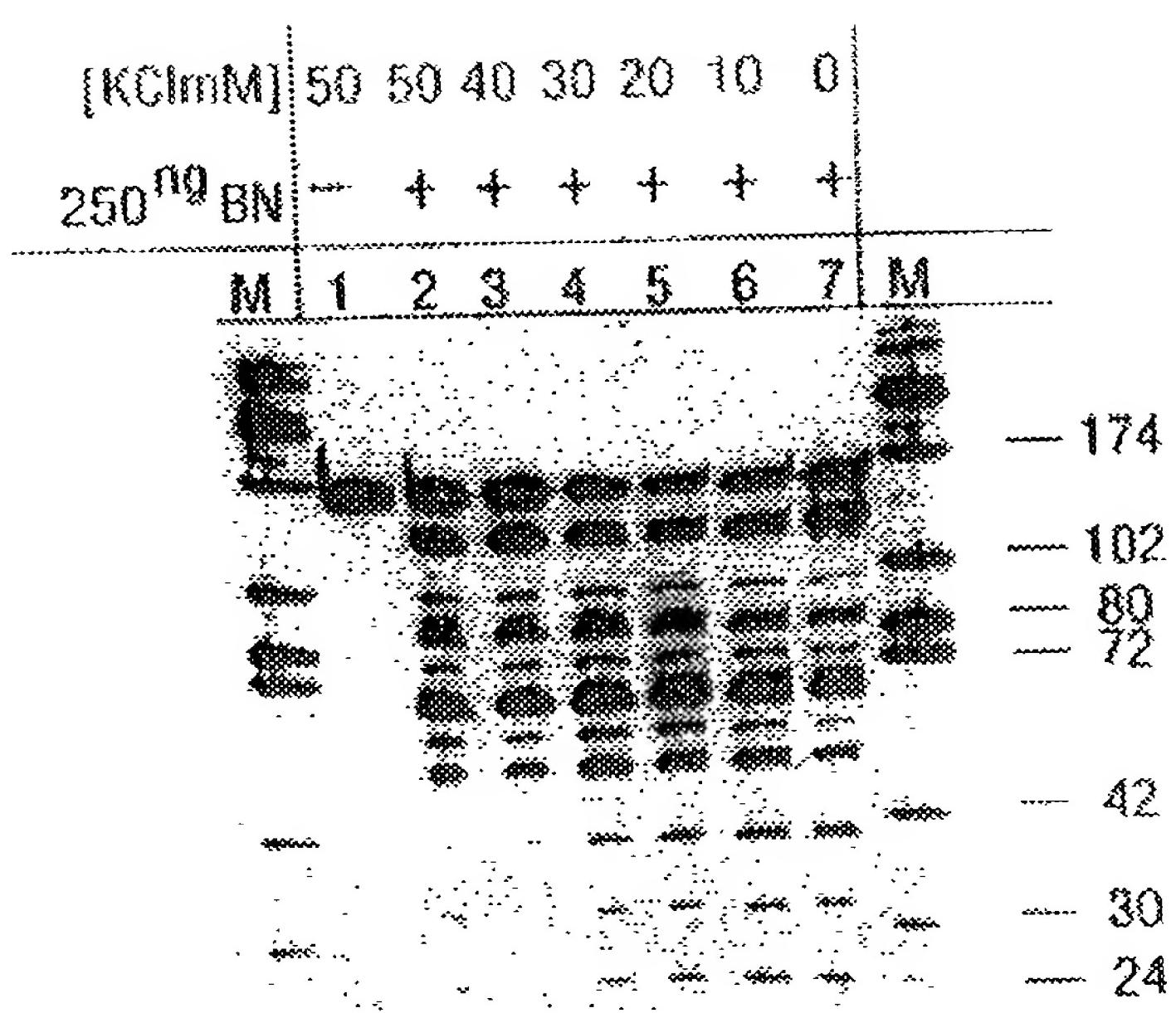


FIG. 36

10 <1 1 5 10

TIME (MIN.)
CLEAVASE™BN:

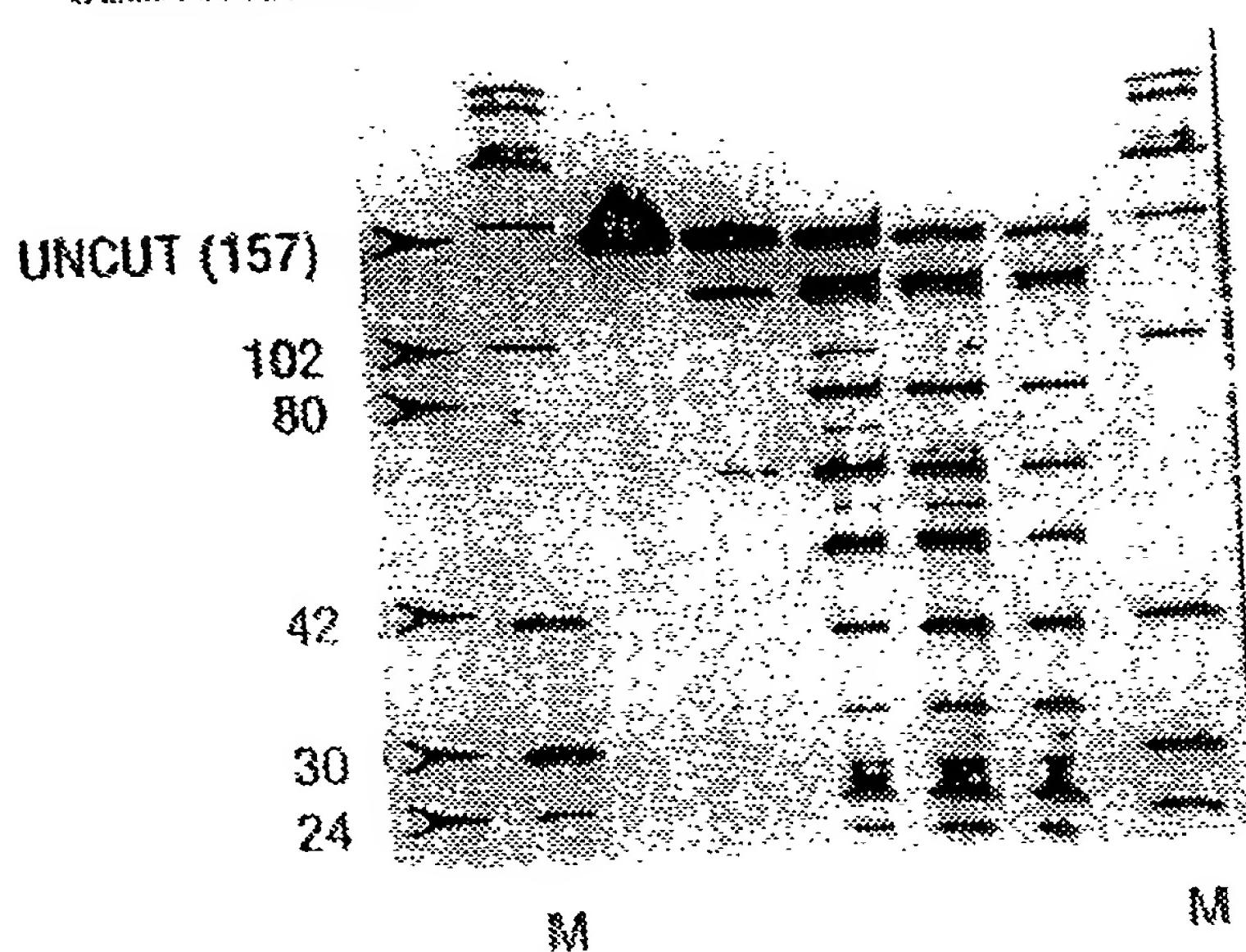


FIG. 36

TEMPERATURE (°C)	55	80	55	60	65	70	75	80
CLEAVAGE ^a (%)	—	—	+	+	+	+	—	+

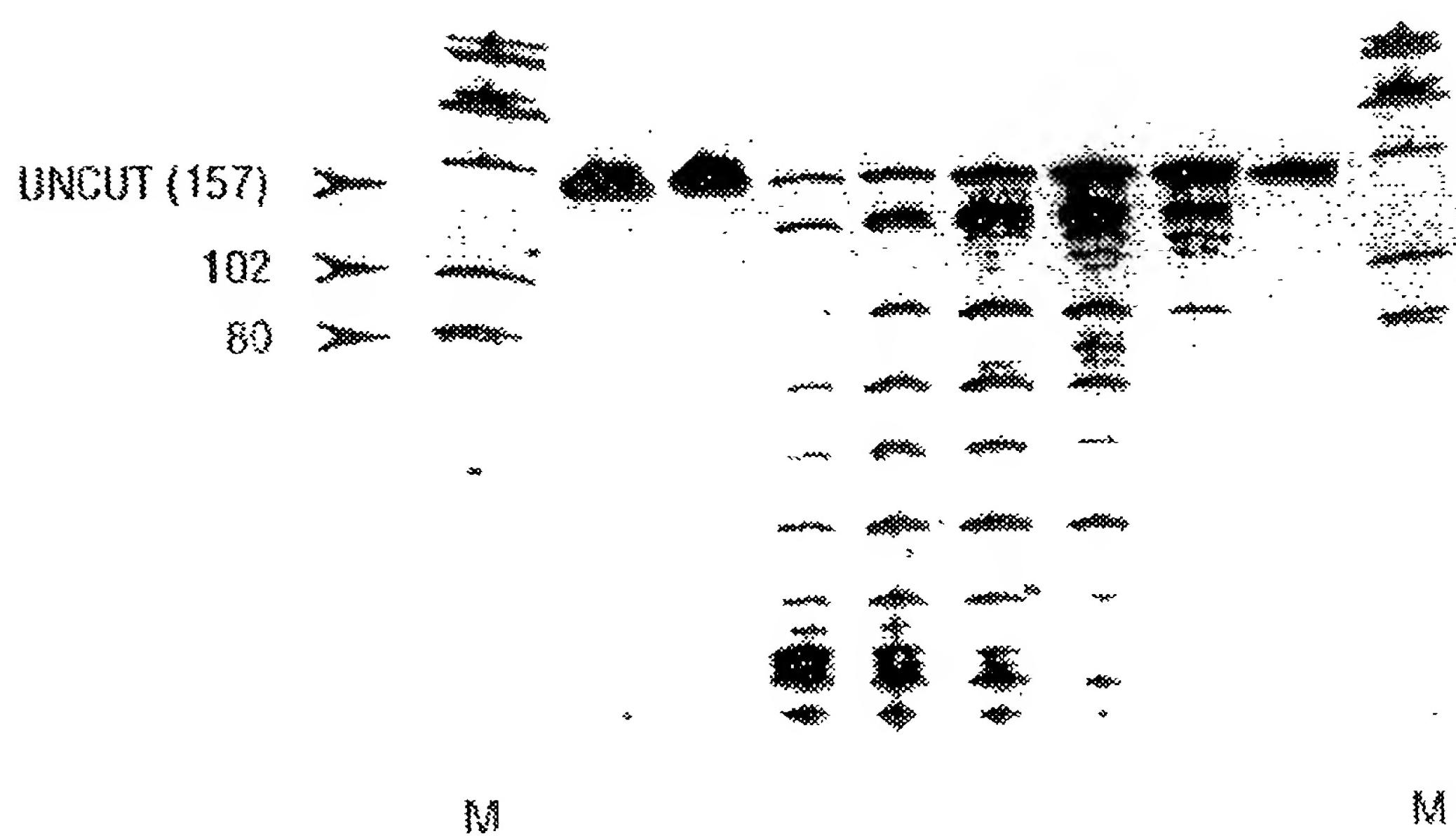


FIG. 37

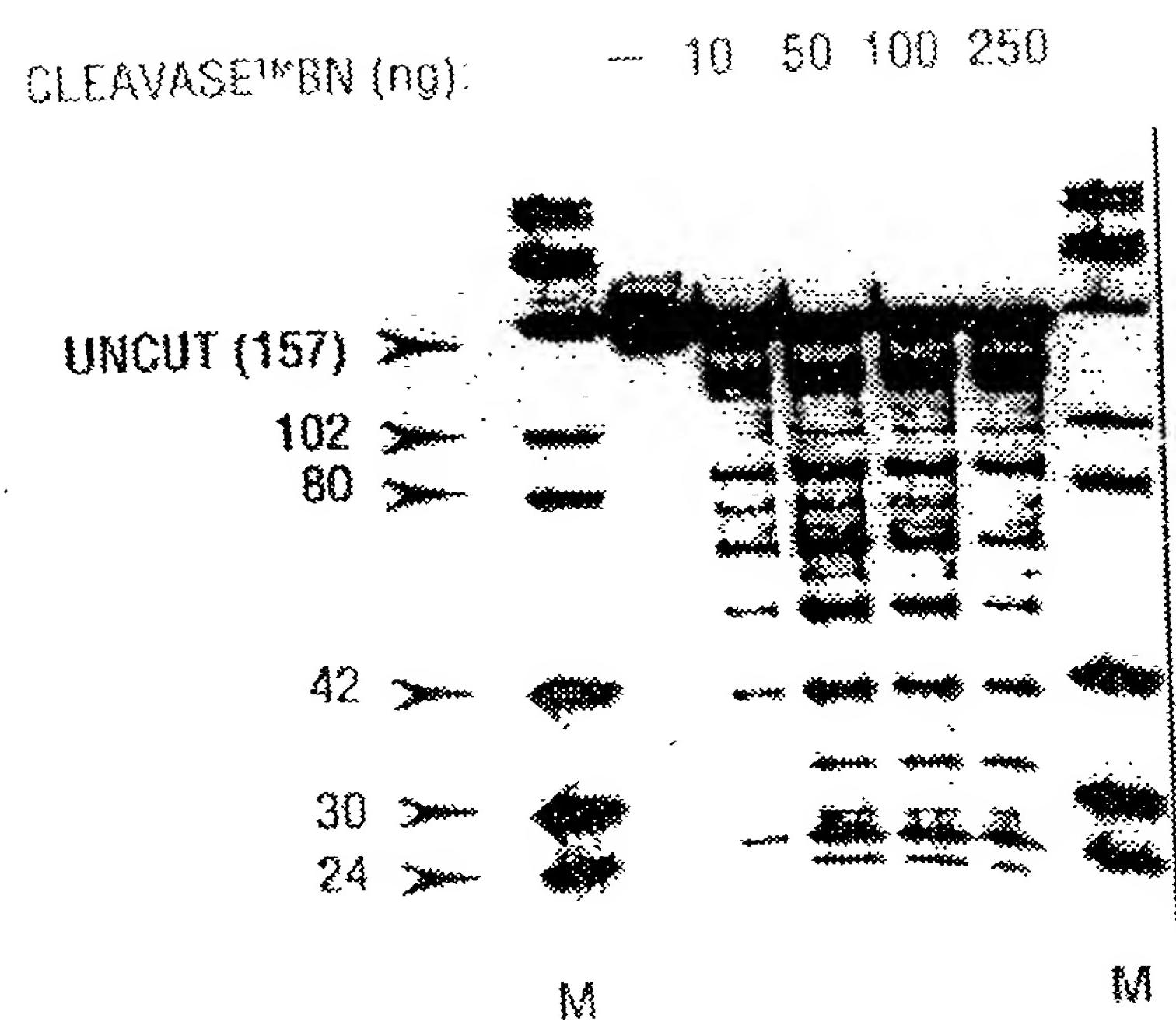


FIG. 38

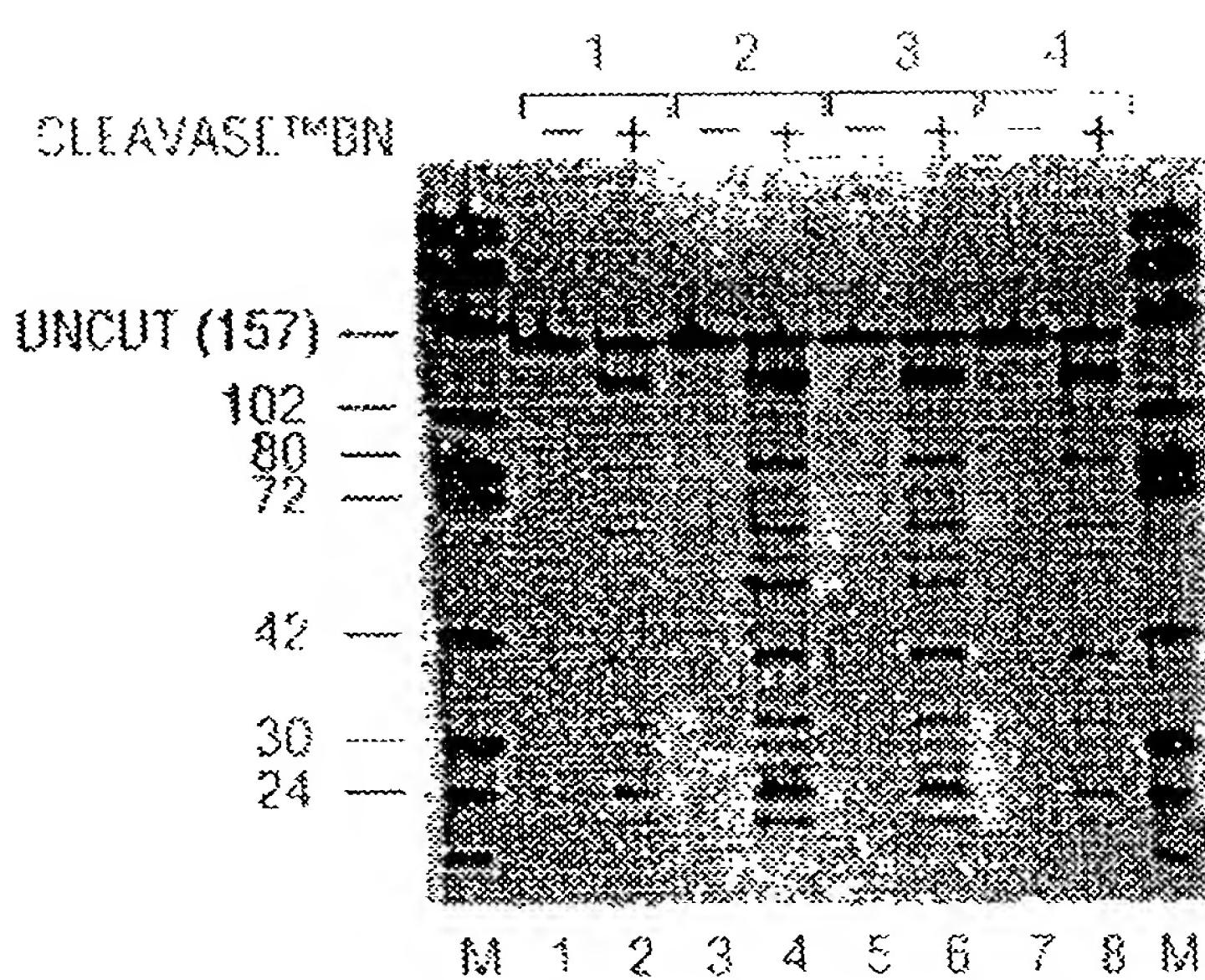


FIG. 39

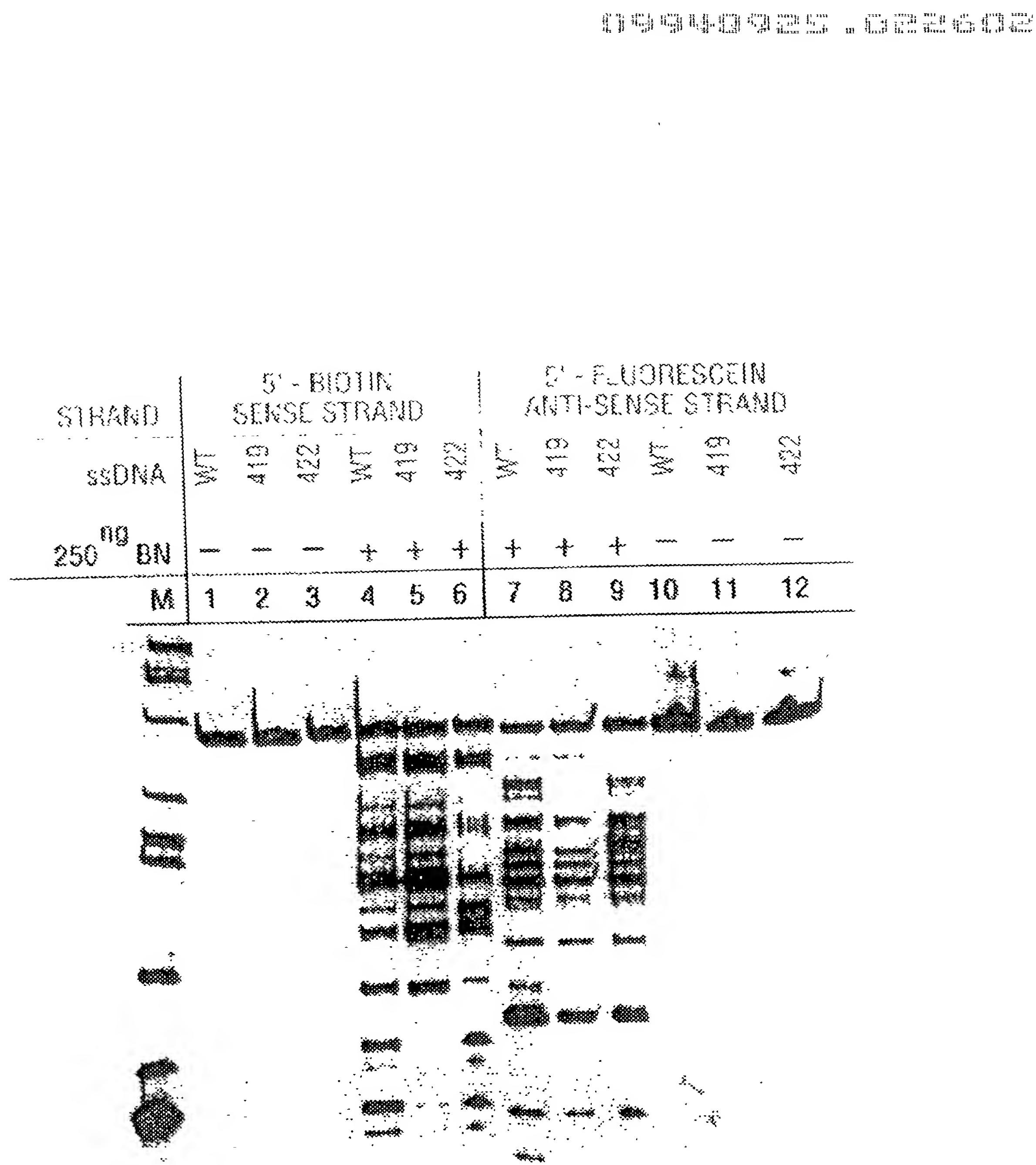


FIG. 40

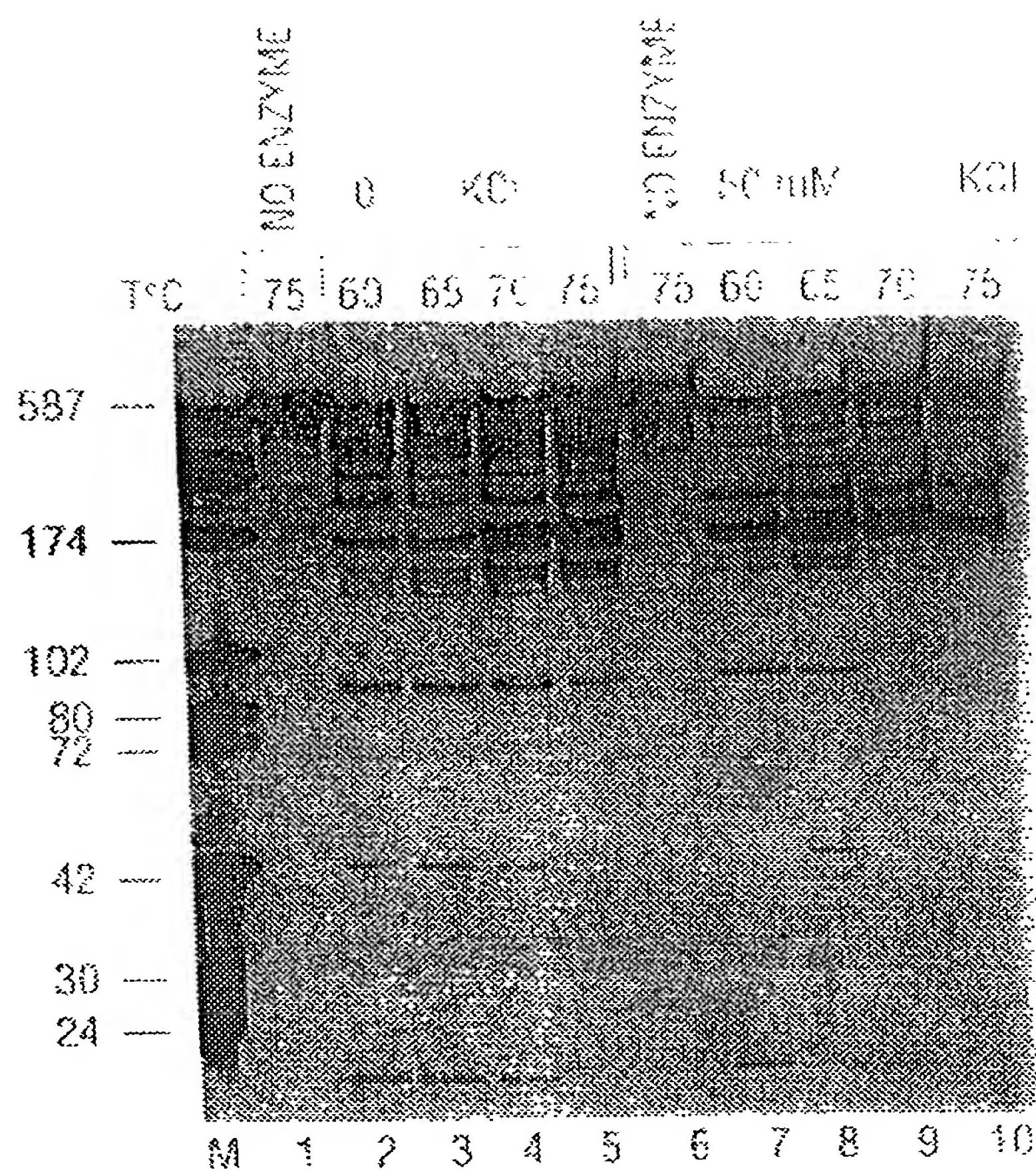


FIG. 41

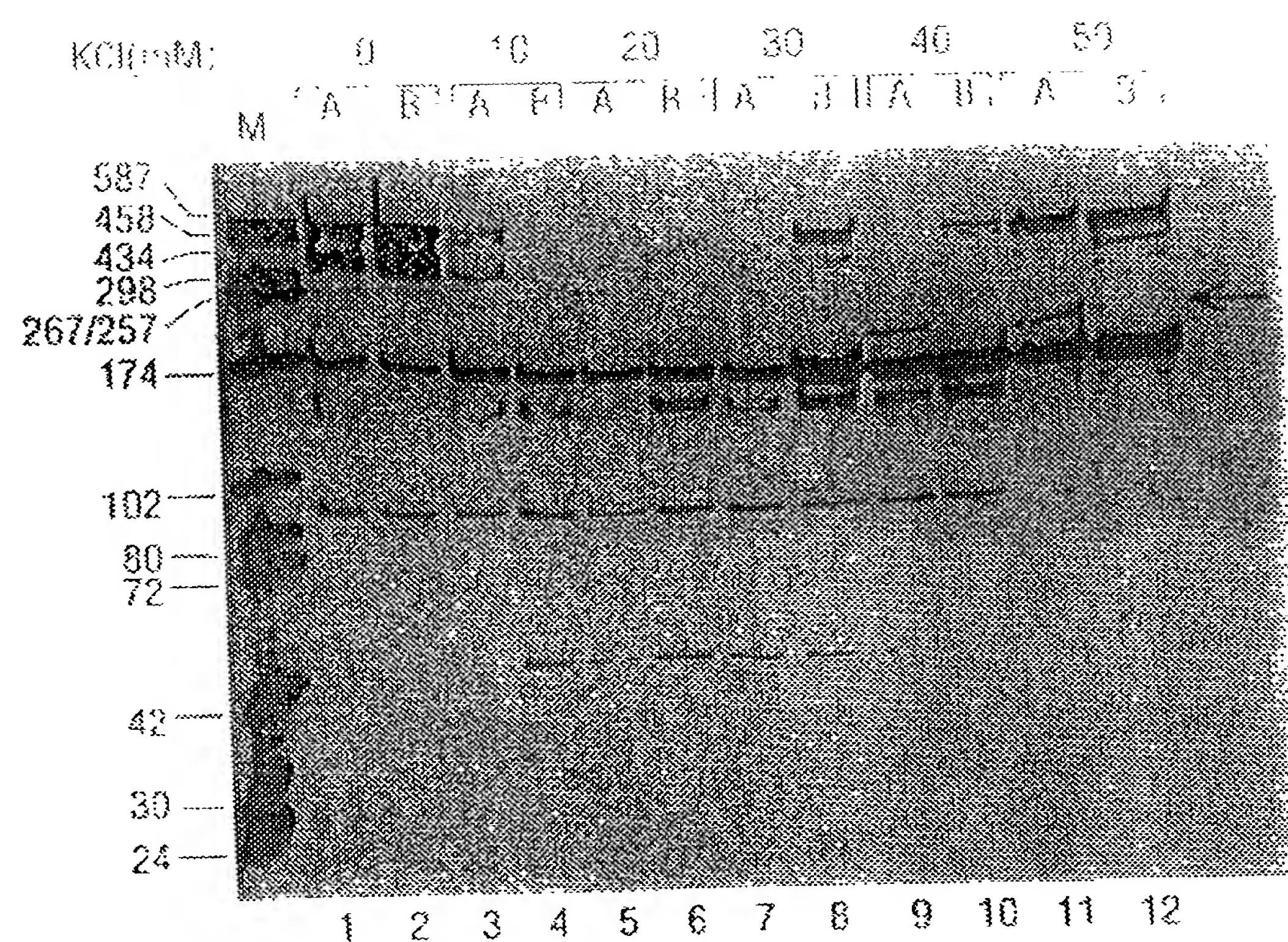


FIG. 42

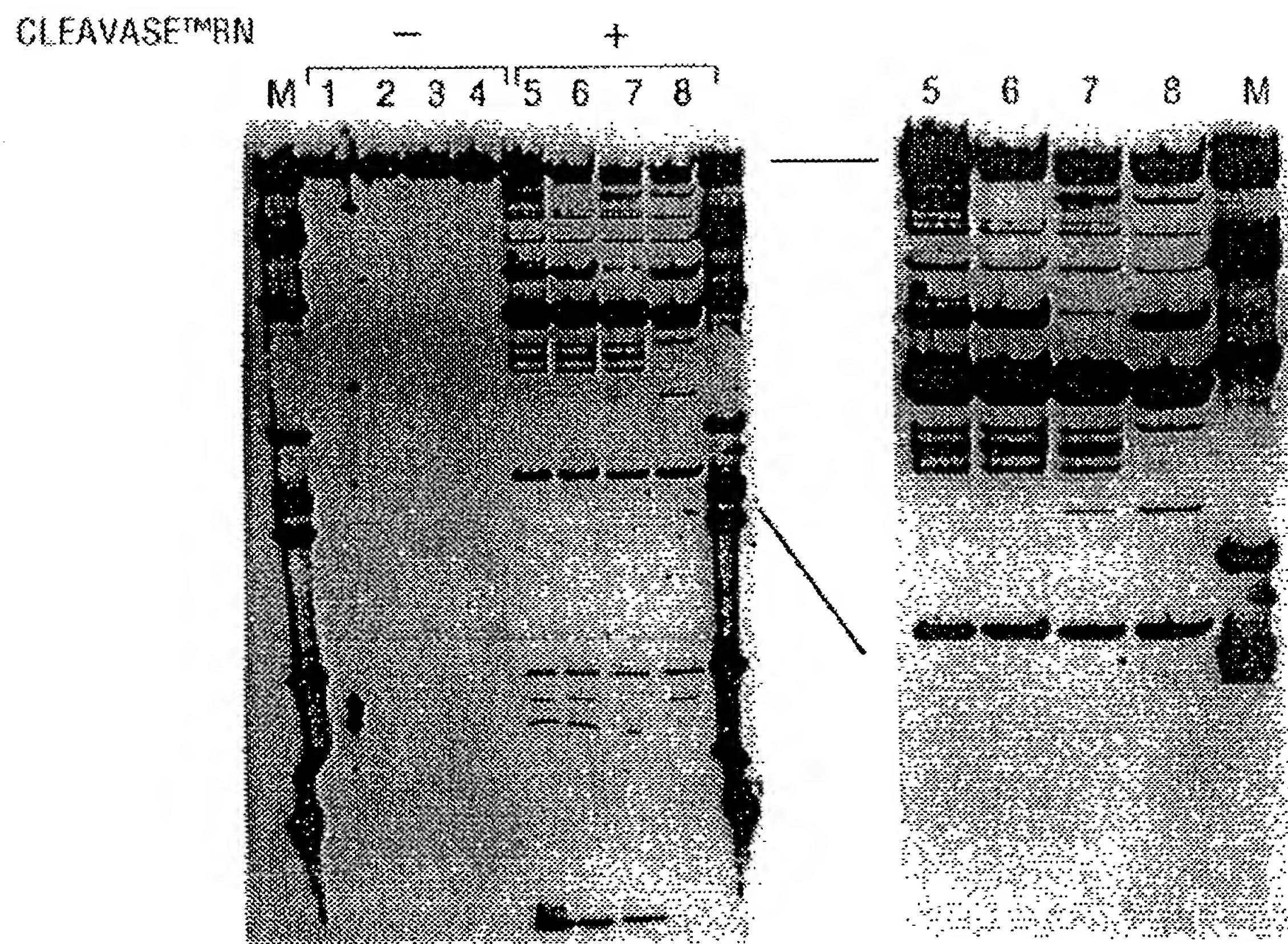


FIG. 43

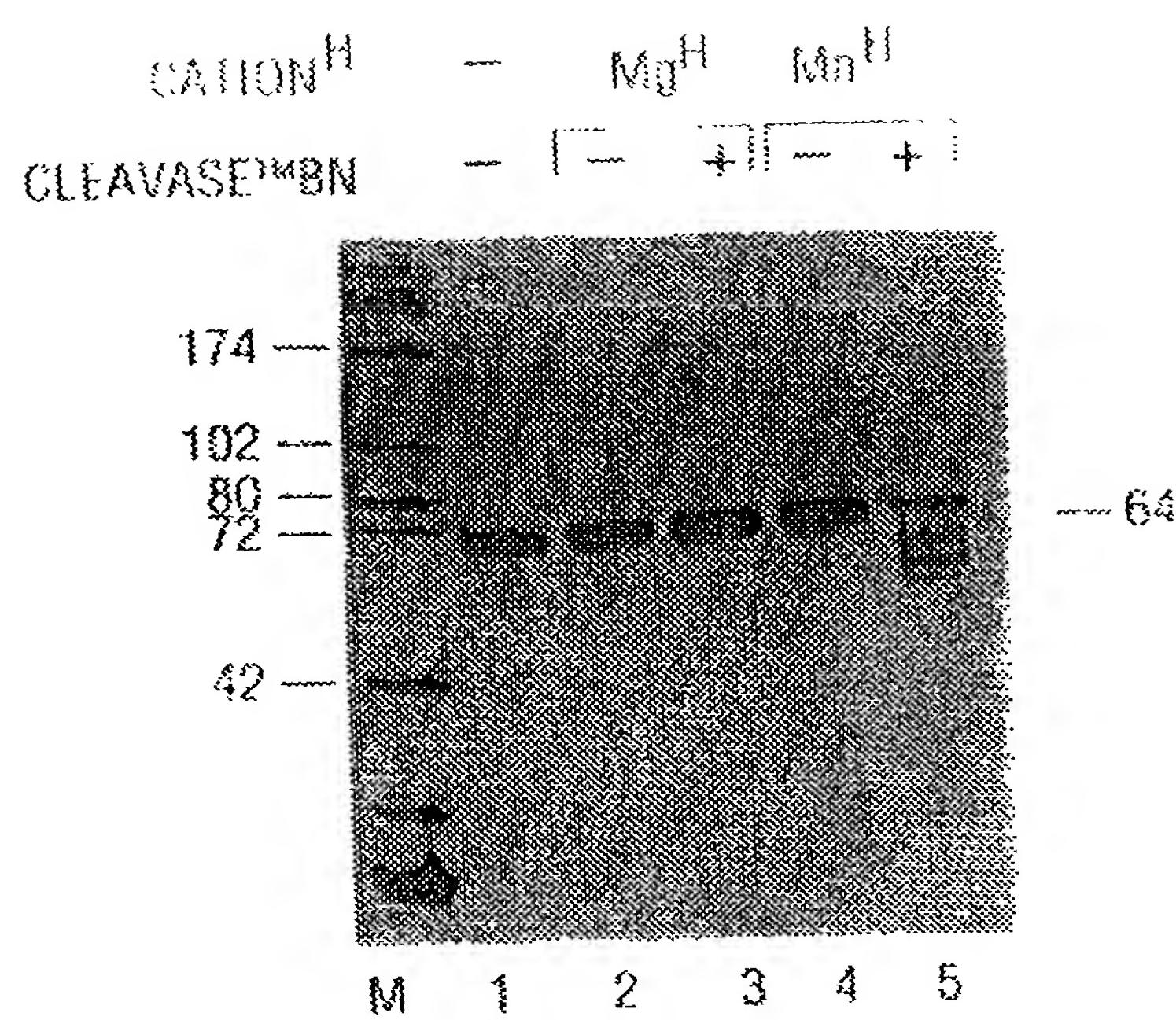


FIG. 44

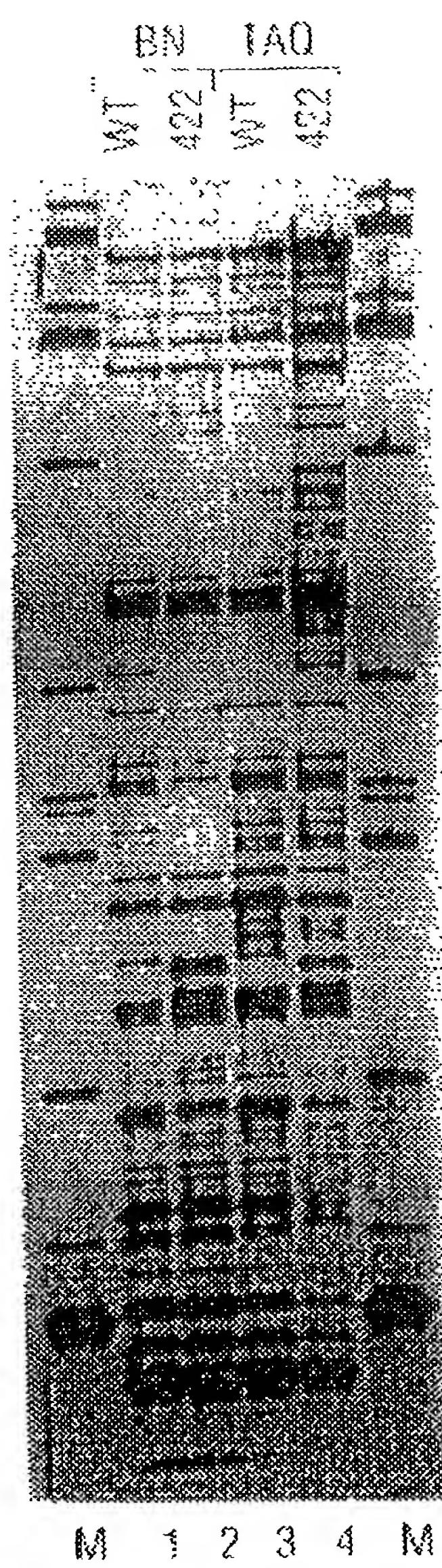


FIG. 45

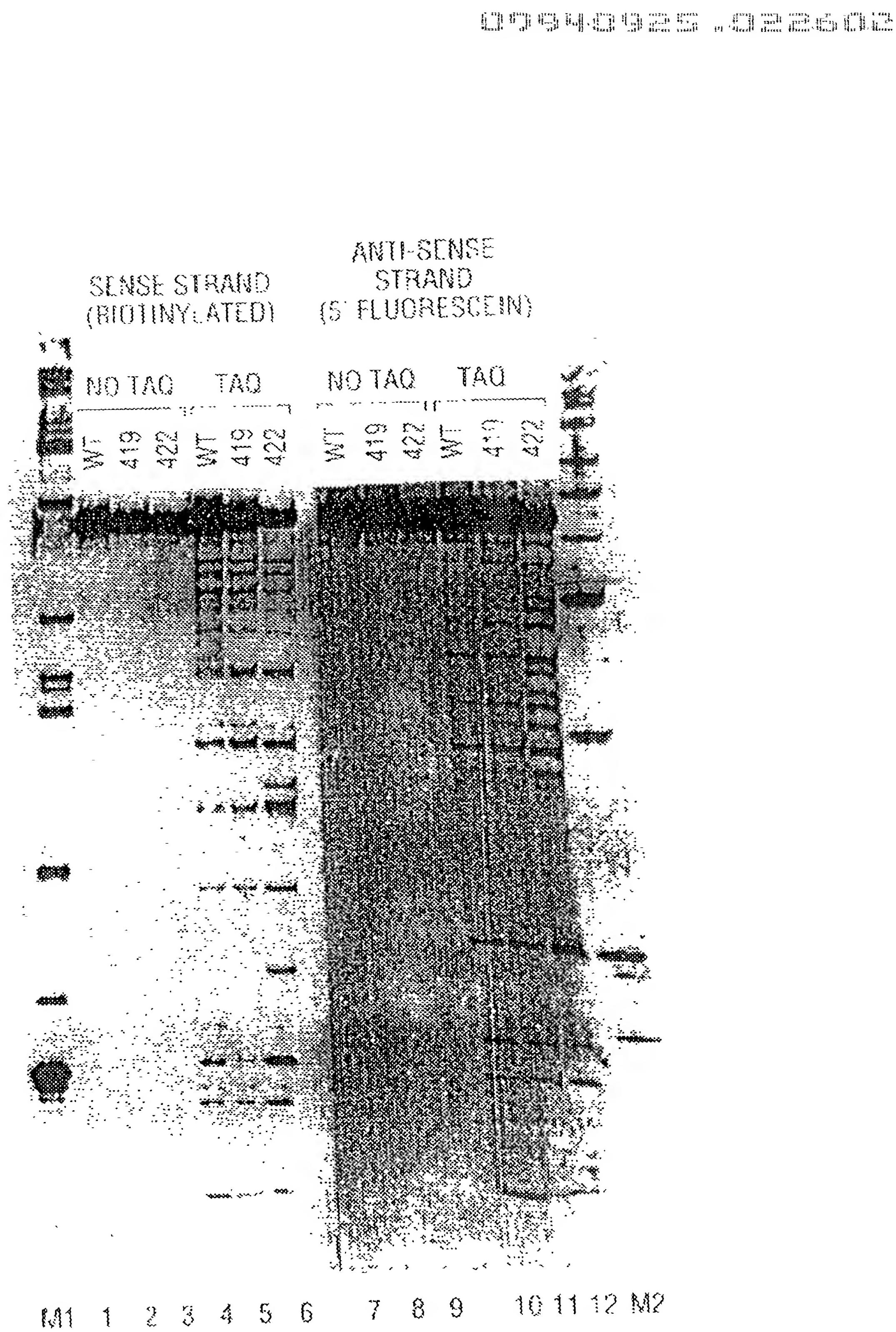


FIG. 46

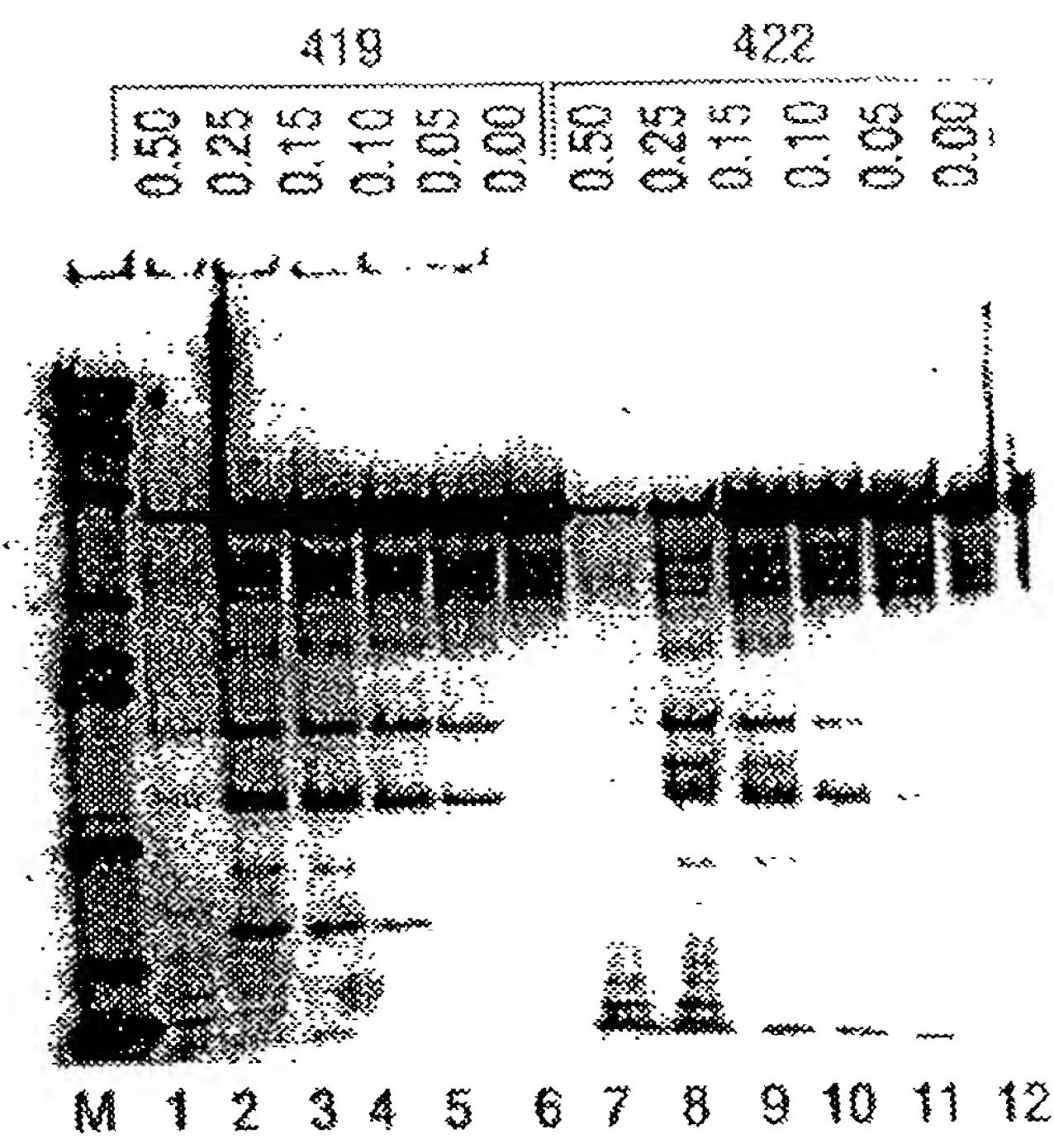


FIG. 47

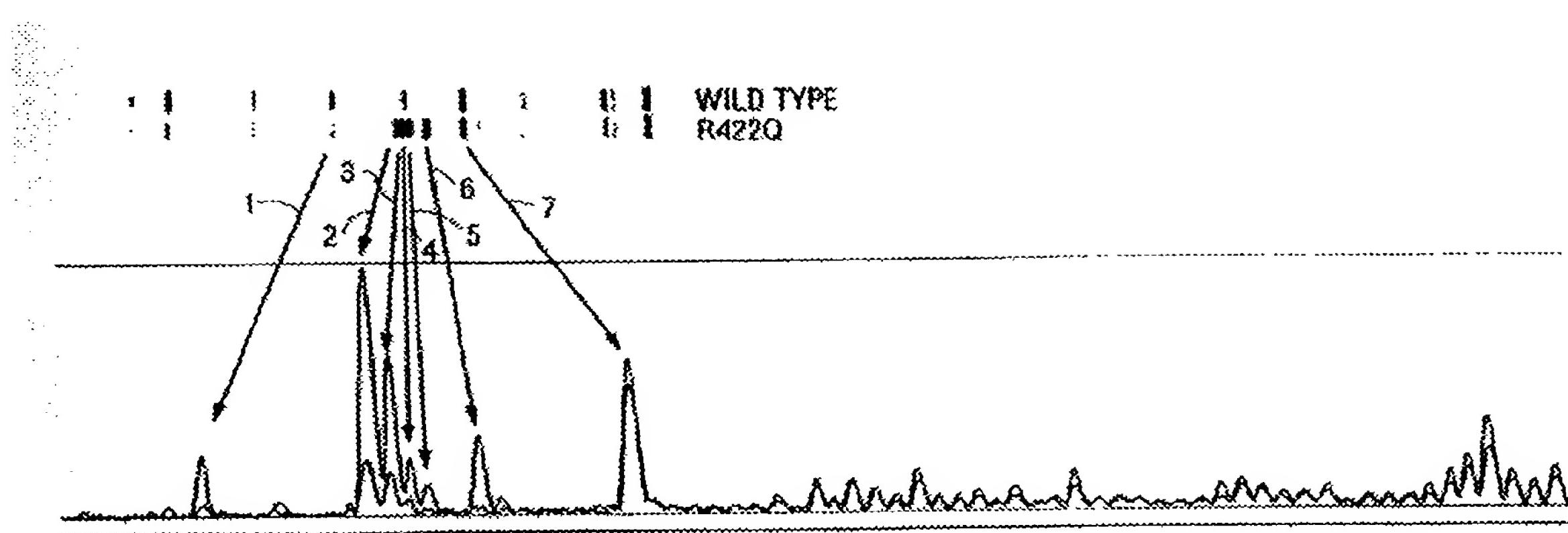


FIG. 48

FIG. 49A

50
L.100.8-1 5'GGCTGACAAGGAAGAAACTCCGCTGAGACAGCAGGGACTTTCCACAAAGGGG
(SEQ ID NO.: 76) 3'CCGACTGTTCTTCCCTTGAGCCACTCTGTGTCGTCCTGAAAGGTGTTCCCC

L.46.16-10 5'GGCTGACAAGGAAGAAACTCGGCTGAGATAGCAGGGACTTTCCACAAAGGGG
(SEQ ID NO.: 77) 3'CCGACTGTTCTTCCCTTGAGCCACTCTGTGTCGTCCTGAAAGGTGTTCCCC

L.46.16-12 5'GGCTGACAAGGAAGAAACTCGGCTGAGATAGCAGGGACTTTCCACAAAGGGG
(SEQ ID NO.: 78) 3'CCGACTGTTCTTCCCTTGAGCCACTCTGTGTCGTCCTGAAAGGTGTTCCCC

L19.16-3 5'GGCTGACAAGGAAGAAACTCGGCTGAGACAGCAGGGACTTTCCACAAAGGGG
(SEQ ID NO.: 79) 3'CCGACTGTTCTTCCCTTGAGCCACTCTGTGTCGTCCTGAAAGGTGTTCCCC

L.CEM/251 5'GGCTGACAAGGAAGAAACTCGGCTGAAACAGCAGGGACTTTCCACAAAGGGG
(SEQ ID NO.: 80) 3'CCGACTGTTCTTCCCTTGAGCCACTCTGTGTCGTCCTGAAAGGTGTTCCCC

L.36.8-3 5'GGCTGACAAGGAAGAAACTCGGCTGAGACAGCAGGGACTTTCCACAAAGGGG
(SEQ ID NO.: 81) 3'CCGACTGTTCTTCCCTTGAGCCACTCTGTGTCGTCCTGAAAGGTGTTCCCC

100
ATGTTACGGGAGGTACTGGGAGGGACGGCCACTCTCT
TACAATGCCCTCCATGACCCTCAGCCCTTGCGGGTGAAGAGA

L.100.8-1 (SEQ ID NO: 76)
ATGTTATGGGAGG-----AGCCGGTGGAACACCCCACCTTTCT
TACAATAACCCCTCC-----TCGGCCAGCCCTTGCGGGTGAAGAGA

L.46.16-10 (SEQ ID NO: 77)
ATGTTATGGGAGG-----AGCCGGTGGAACACCCCACCTTTCT
TACAATAACCCCTCC-----TCGGCCAGCCCTTGCGGGTGAAGAGA

L.46.16-12 (SEQ ID NO: 78)
ATGTTACGGGAGGTACTGGGAGGGAGCCGGTGGAACACCCCACCTTTCT
TACAATGCCCTCCATGACCCTCAGCCCTTGCGGGTGAAGAGA

L.19.16-3 (SEQ ID NO: 19)
ATGTTACGGGAGGTACTGGAAAGGAAGGGAGCCGGTGGAACACCCCACCTTTCT
TACAATGCCCTCCATGACCCTCAGCCCTTGCGGGTGAAGAGA

L.CEM/251 (SEQ ID NO: 80)
ATGTTACGGGAGGTACTGGGAGGGAGCCGGTGGAACACCCCACCTCTCT
TACAATGCCCTCCATGACCCTCAGCCCTTGCGGGTGAAGAGA

L.36.8-3 (SEQ ID NO: 81)
ATGTTACGGGAGGTACTGGGAGGGAGCCGGTGGAACACCCCACCTCTCT
TACAATGCCCTCCATGACCCTCAGCCCTTGCGGGTGAAGAGA

FIG. 49B

L. 100. 8-1 5' TGATGATAAATACTCACTGCATTGGCTCTGTTATTCA GTCGCTCTGGGA 3' ACTACATATTAGTGGACGTAAAGGAGACATAAGTCAGCAGACCT	L. 46. 16-10 5' TGATGATAAATACTCACTGCATTGGCTCTGTTATTCA GTCGCTCTGGGA 3' ACTACATATTAGTGGACGTAAAGGAGACATAAGTCAGCAGACCT	L. 46. 16-12 5' TGATGATAAATACTCACTGCATTGGCTCTGTTATTCA GTCGCTCTGGGA 3' ACCACATATTAGTGGACGTAAAGGAGACATAAGTCAGCAGACCT	L. 19. 16-3 5' TGATGATAAATACTCACTGCATTGGCTCTGTTATTCA GTCGCTCTGGGA 3' ACTACATATTAGTGGACGTAAAGGAGACATAAGTCAGCAGACCT	L. CEM/251 5' TGATGATAAATACTCACTGCATTGGCTCTGTTATTCA GTCGCTCTGGGA 3' ACTACATATTAGTGGACGTAAAGGAGACATAAGTCAGCAGACCT	L. 36. 8-3 5' TGATGATAAATACTCACTGCATTGGCTCTGTTATTCA GTCGCTCTGGGA 3' ACTACATATTAGTGGACGTAAAGGAGACATAAGTCAGCAGACCT
---	--	--	---	--	--

FIG. 49C

FIG. 49D

200
L. 100.8-1 GAGGCTGGCAGATTGAGCCCTGGAGGTCTCTCCAGGACTAGCAGGTAG
 CTCCGACCGTCTAACTCGGGACCCCTCAAGAGGGTGGTGAATCGTCCATC

L. 46.16-10 GAGGCTGGCAGATTGAGCCCTGGAGGTCTCTCCAGGACTAGCAGGTAG
 CTCCGACCGTCTAACTCGGGACCCCTCAAGAGGGTGGTGAATCGTCCATC

L. 46.16-12 GAGGCTGGCAGATTGAGCCCTGGAGGTCTCTCCAGGACTAGCAGGTAG
 CTCCGACCGTCTAACTCGGGACCCCTCAAGAGGGTGGTGAATCGTCCATC

L. 19.16-3 GAGGCTGGCAGATTGAGCCCTGGAGGTCTCTCCAGGACTAGCAGGTAG
 CTCCGACCGTCTAACTCGGGACCCCTCAAGAGGGTGGTGAATCGTCCATC

L. CEM/251 GAGGCTGGCAGATTGAGCCCTGGAGGTCTCTCCAGGACTAGCAGGTAG
 CTCCGACCGTCTAACTCGGGACCCCTCAAGAGGGTGGTGAATCGTCCATC

L. 36.8-3 GAGGCTGGCAGATTGAGCCCTAGGAGGTCTCTCCAGGACTAGCAGGTAG
 CTCCGACCGTCTAACTCGGGATCCTGGTGAAGAGGGTGGTGAATCGTCCATC

L. 100. 8 -1 5'AGCCCTGGGTGTTCCCTGCTAGACTCTCACCGCACTTGGCCGGTGGTGGG
 (SEQ ID NO: 76) 3'TCGGACCCACAAGGGACCATCTGAGAGTGGTCGTGAAACGCCACCC

L. 46.16-10 5'AGCCCTGGGTGTTCCCTGCTAGACTCTCACCGCACTTAGCCAGTAGCTGCTGGG
 (SEQ ID NO: 77) 3'TCGGACCCACAAGGGACGATCTGAGAGTGGTCGTGAAATGGTCACCGACCC

L. 46.16-12 5'AGCCCTGGGTGTTCCCTGCTAGACTCTCACCGCACTTGGCCAGTAGCTGCTGGG
 (SEQ ID NO: 78) 3'TCGGACCCACAAGGGACGATCTGAGAGTGGTCGTGAAACGGTCAACGCCACCC

L. 19.16-3 5'AGCCCTGGGTGTTCCCTGCTAGACTCTCACCGCACTTAGCCGGTGGTGGG
 (SEQ ID NO: 79) 3'TCGGACCCACAAGGGACGATCTGAGAGTGGTCGTGAAACCCGGCACGCCACCC

L. CEM/251 5'AGCCCTGGGTGTTCCCTGCTAGACTCTCACCGCACTTGGCCGGTGGTGGG
 (SEQ ID NO: 80) 3'TCGGACCCACAAGGGACGATCTGAGAGTGGTCGTGAAACGCCACCC

L. 36.8-3 5'AGCCCTGAGTGGTCCCTGCTAAACTCTCACCGCACTTAGCCGGTGGTGGG
 (SEQ ID NO: 81) 3'TCGGACTCACAAAGGGACGATTGAGAGTGGTCGTGAAACCCGGCACGCCACCC

HAIRPIN

FIG. 49E

L. 100. 8 -1
 (SEQ ID NO: 76)
 CAGAGTGGCTCCACCGCTTGCCTTAAGACCTCTCAATAAAGCTGCC
 GTCTCACCGAGGTGGAACGAAACGAATTTCGACGG
 300

L. 46.16-10
 (SEQ ID NO: 77)
 CAGAGTGGCTCCACCGCTTGCCTTAAGACCTCTCAATAAAGCTGCC
 GTCTCACCGAGGTGGAACGAAACGAATTTCGACGG

L. 46.16-12
 (SEQ ID NO: 78)
 CAGAGTGGCTCCACCGCTTGCCTTAAGACCTCTCAATAAAGCTGCC
 GTCTCACCGAGGTGGAACGAAACGAATTTCGACGG

L. 19.16-3
 (SEQ ID NO: 79)
 CAGAGTGGCTCCACCGCTTGCCTTAAGACCTCTCAATAAAGCTGCC
 GTCTCACCGAGGTGGAACGAAACGAATTTCGACGG

L. CEM/251
 (SEQ ID NO: 80)
 CAGAGGGCTCCACCGCTTGCCTTAAGACCTCTCAATAAAGCTGCC
 GTCTCACCGAGGTGGAACGAAACGAATTTCGACGG

L. 36.8-3
 (SEQ ID NO: 81)
 CAGAGGGCTCCACCGCTTGCCTTAAGACCTCTCAATAAAGCTGCC
 GTCTCGGCGAGGTGGAACGAAACGAATTTCGACGG

HAIRPIN

FIG. 49F

FIG. 49G

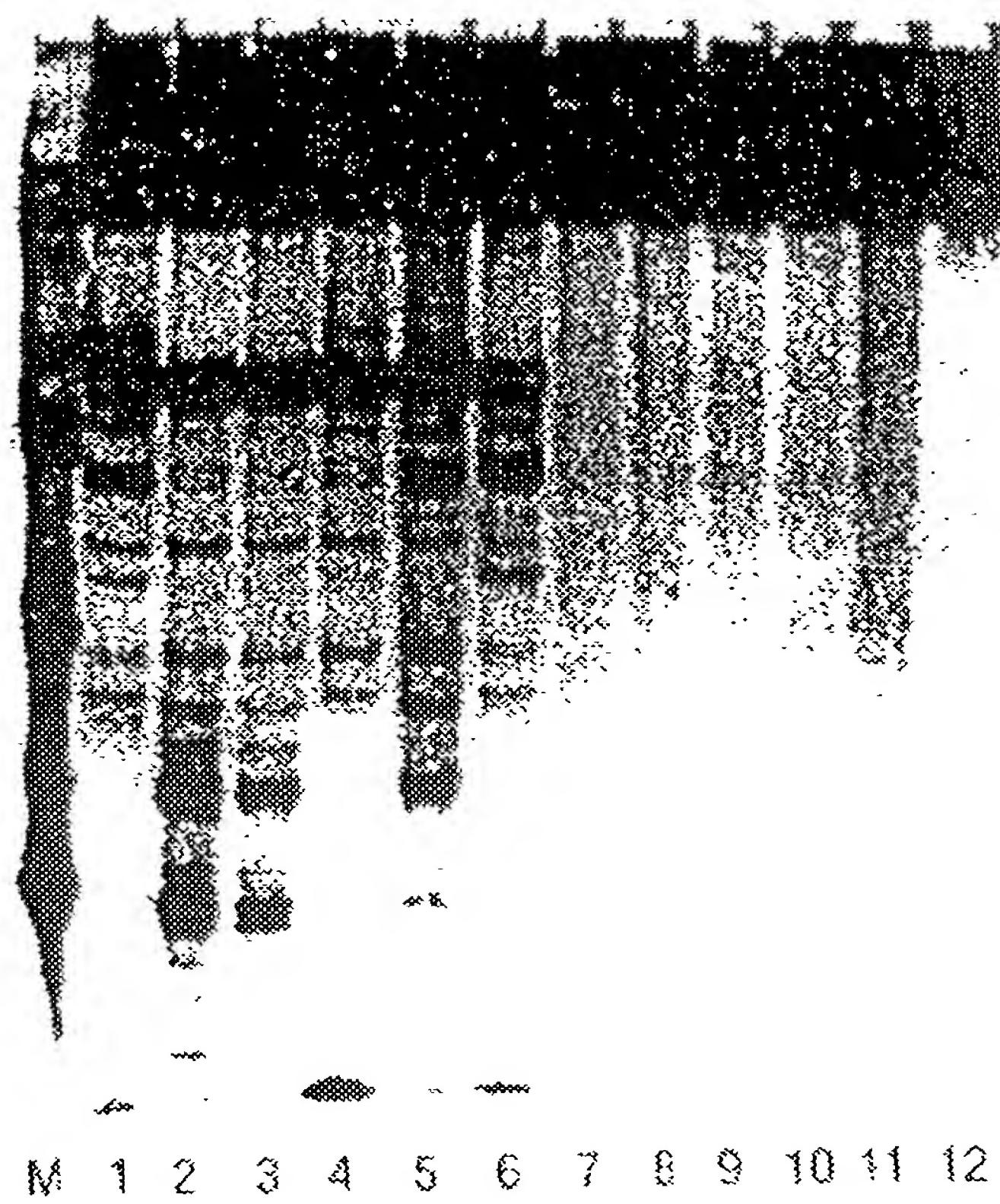
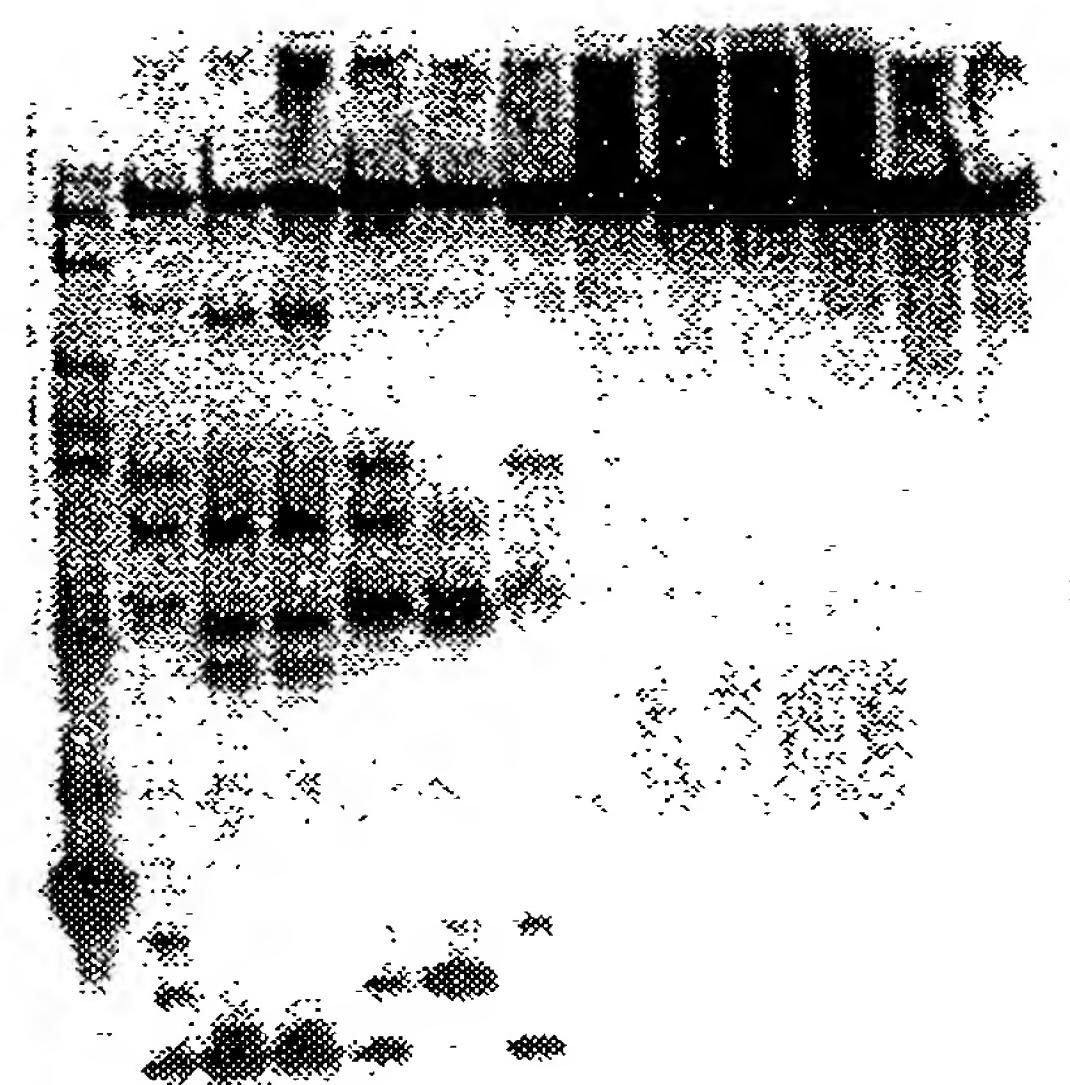


FIG. 50



M 1 2 3 4 5 6 7 8 9 10 11 12

FIG. 51

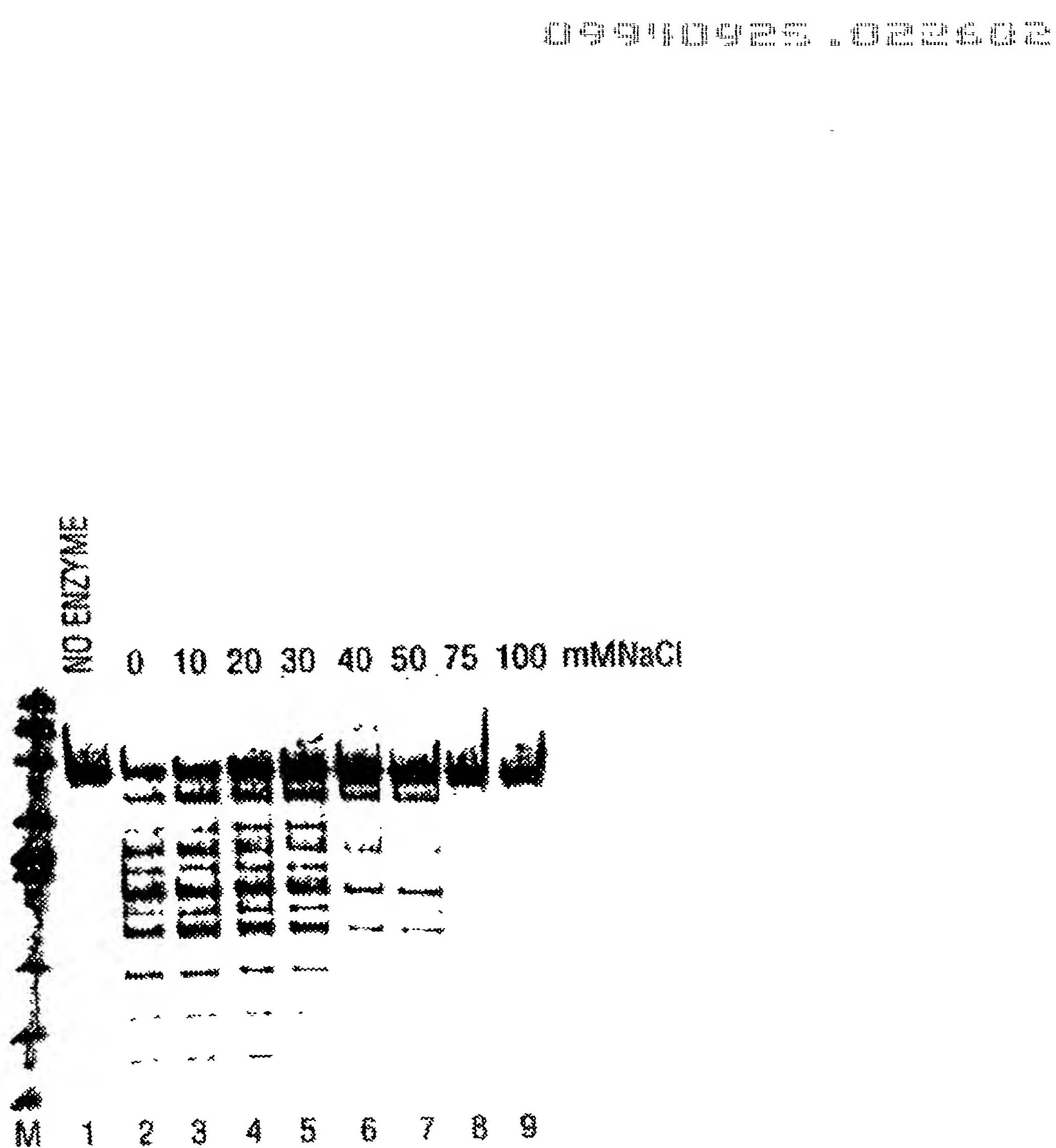


FIG. 52

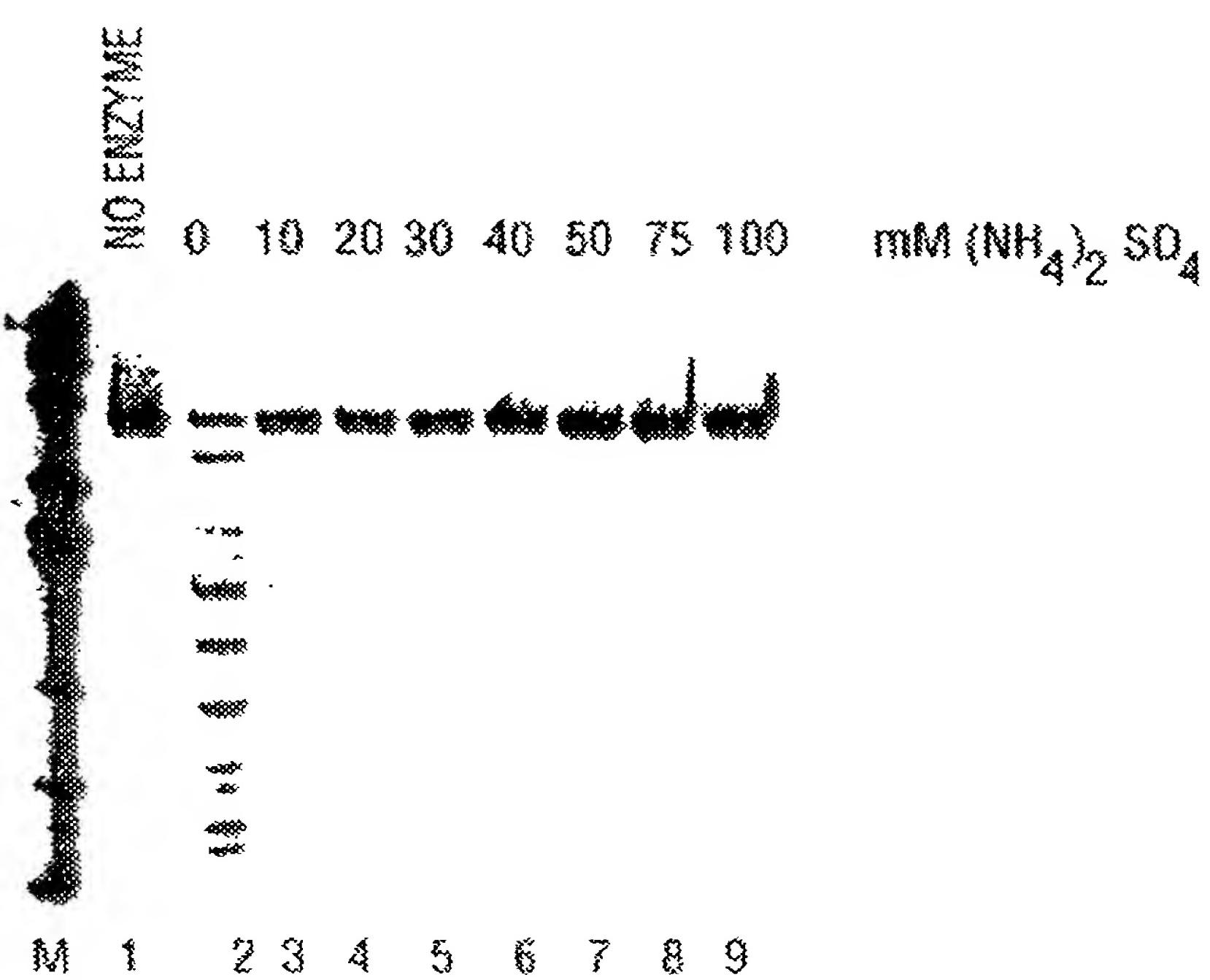


FIG. 53

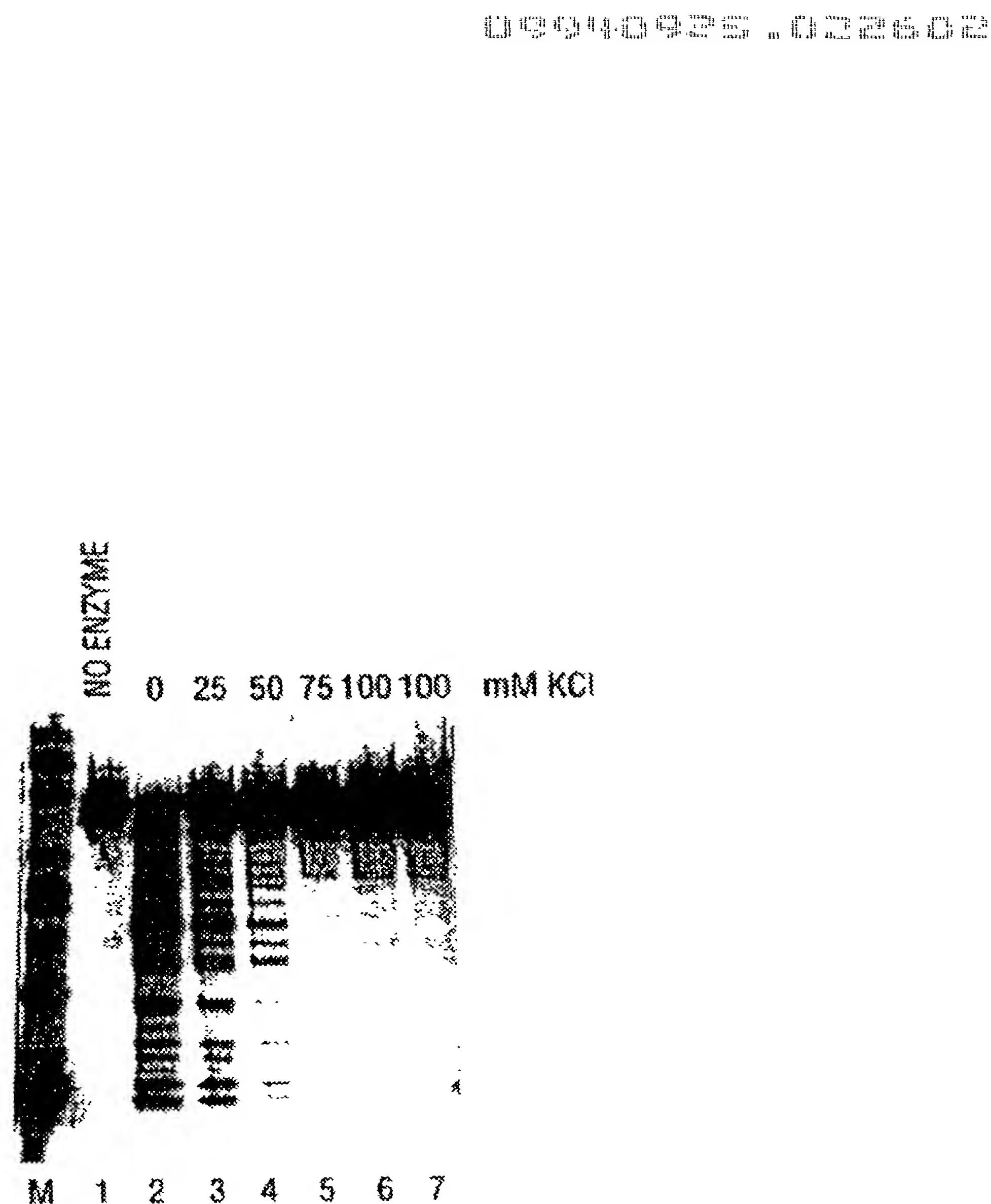


FIG. 54

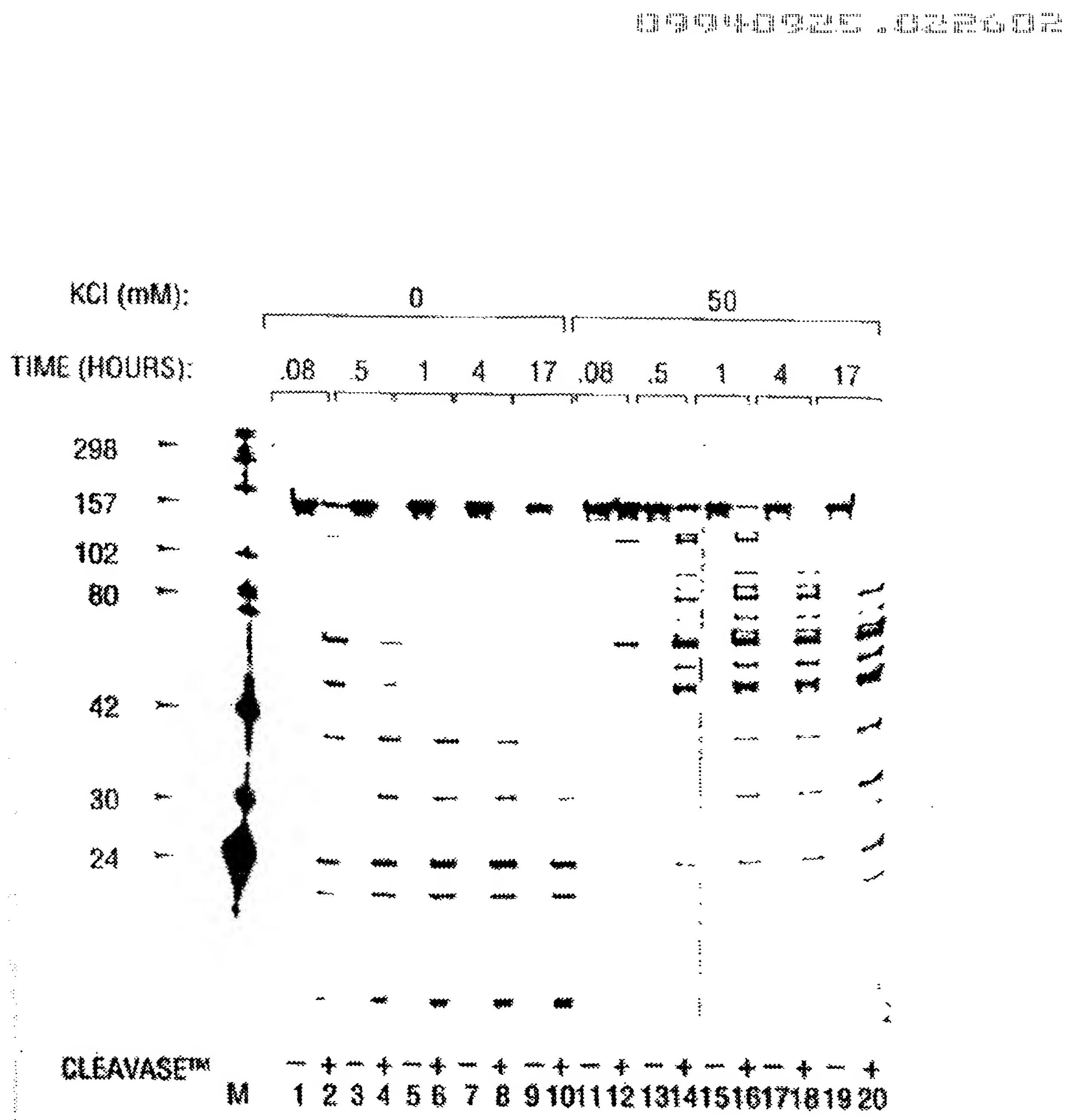


FIG. 55

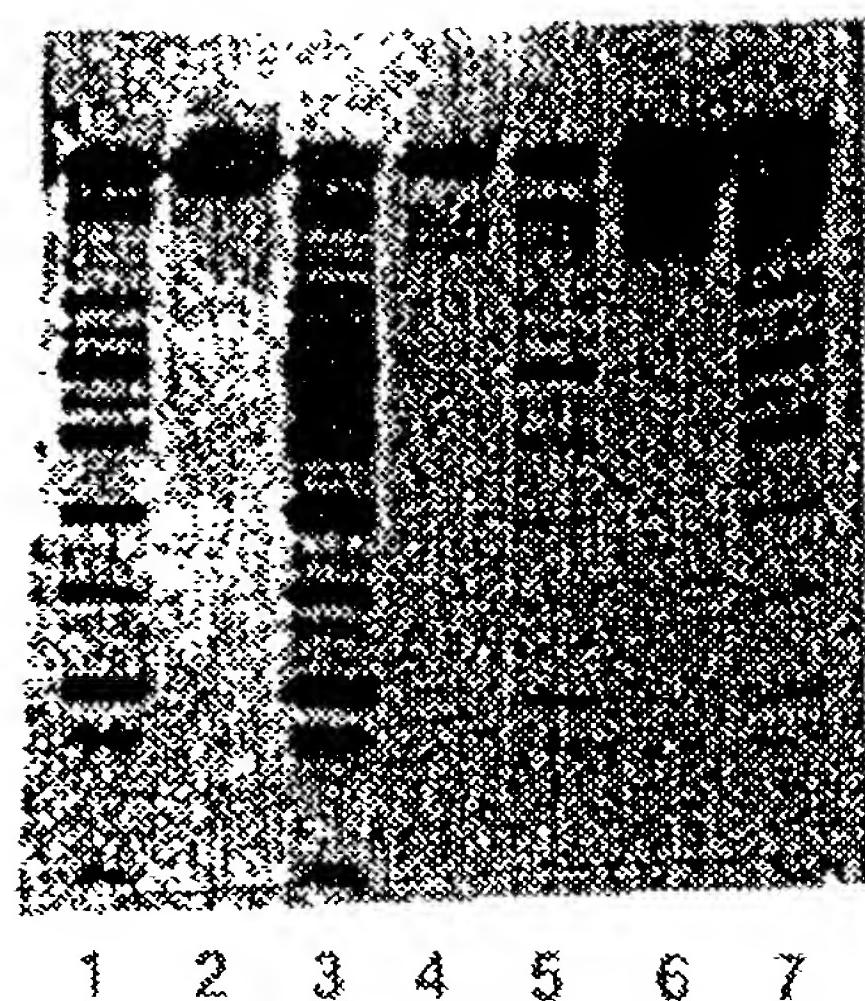


FIG. 56

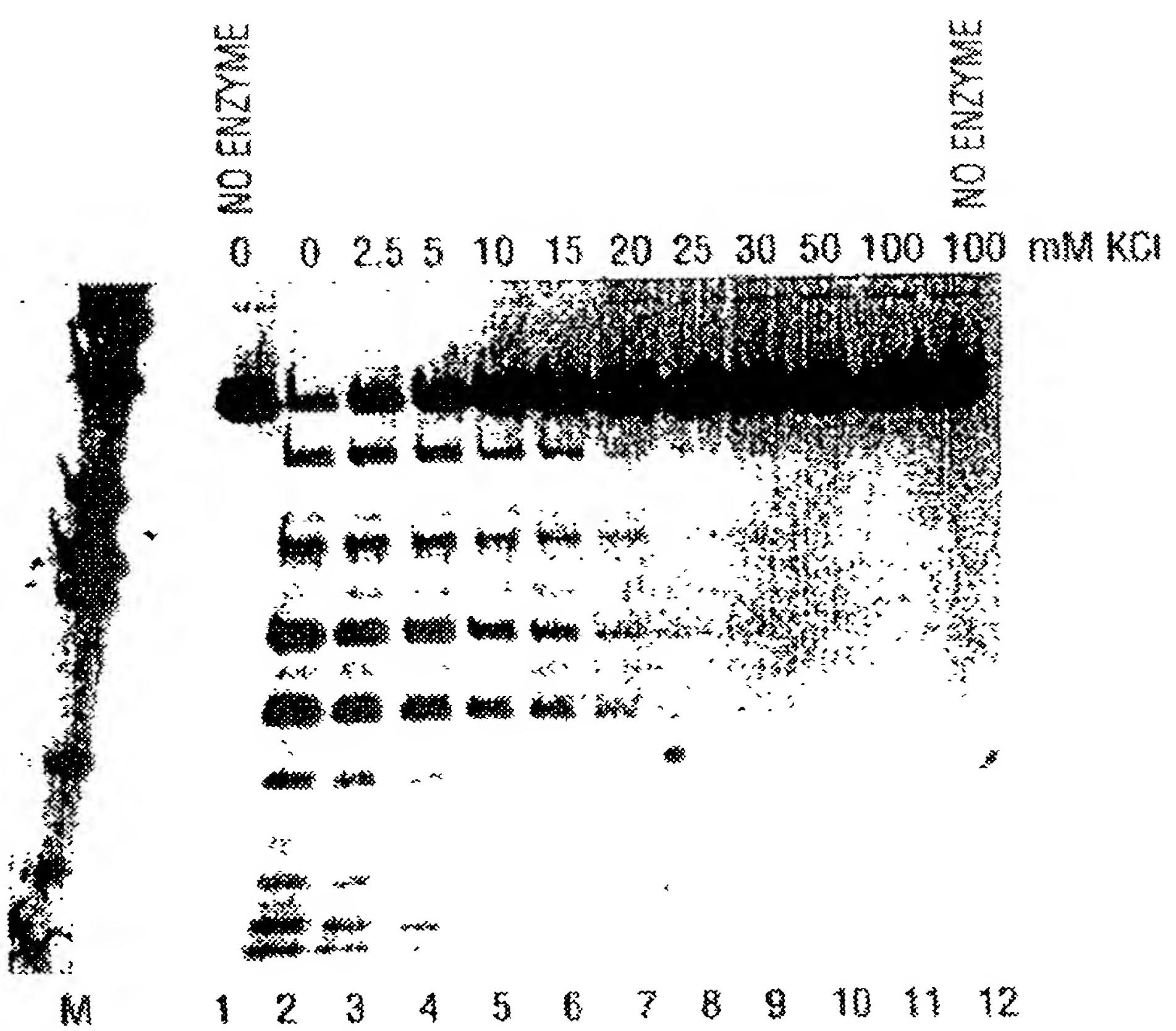


FIG. 57

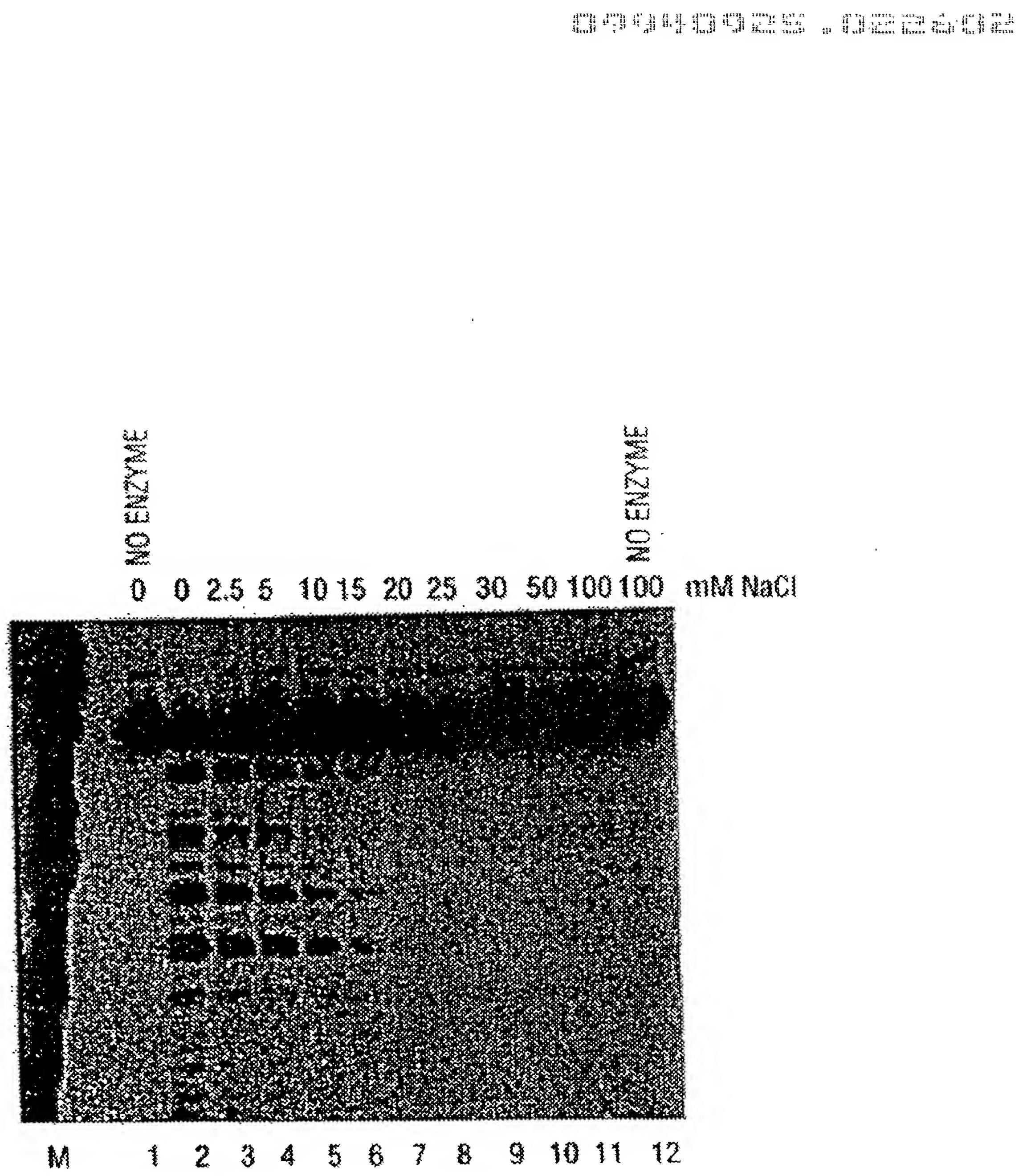


FIG. 58

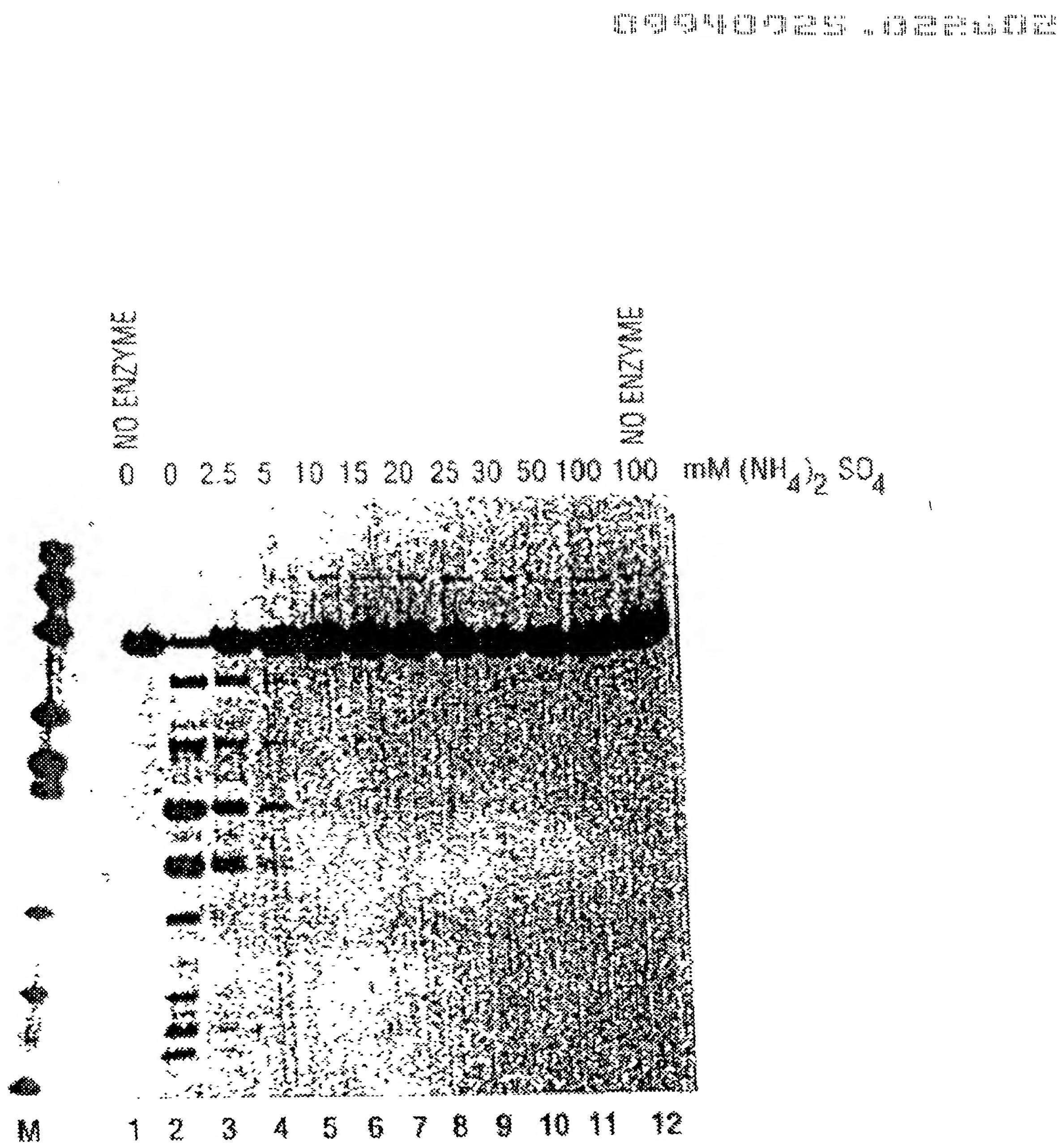


FIG. 59

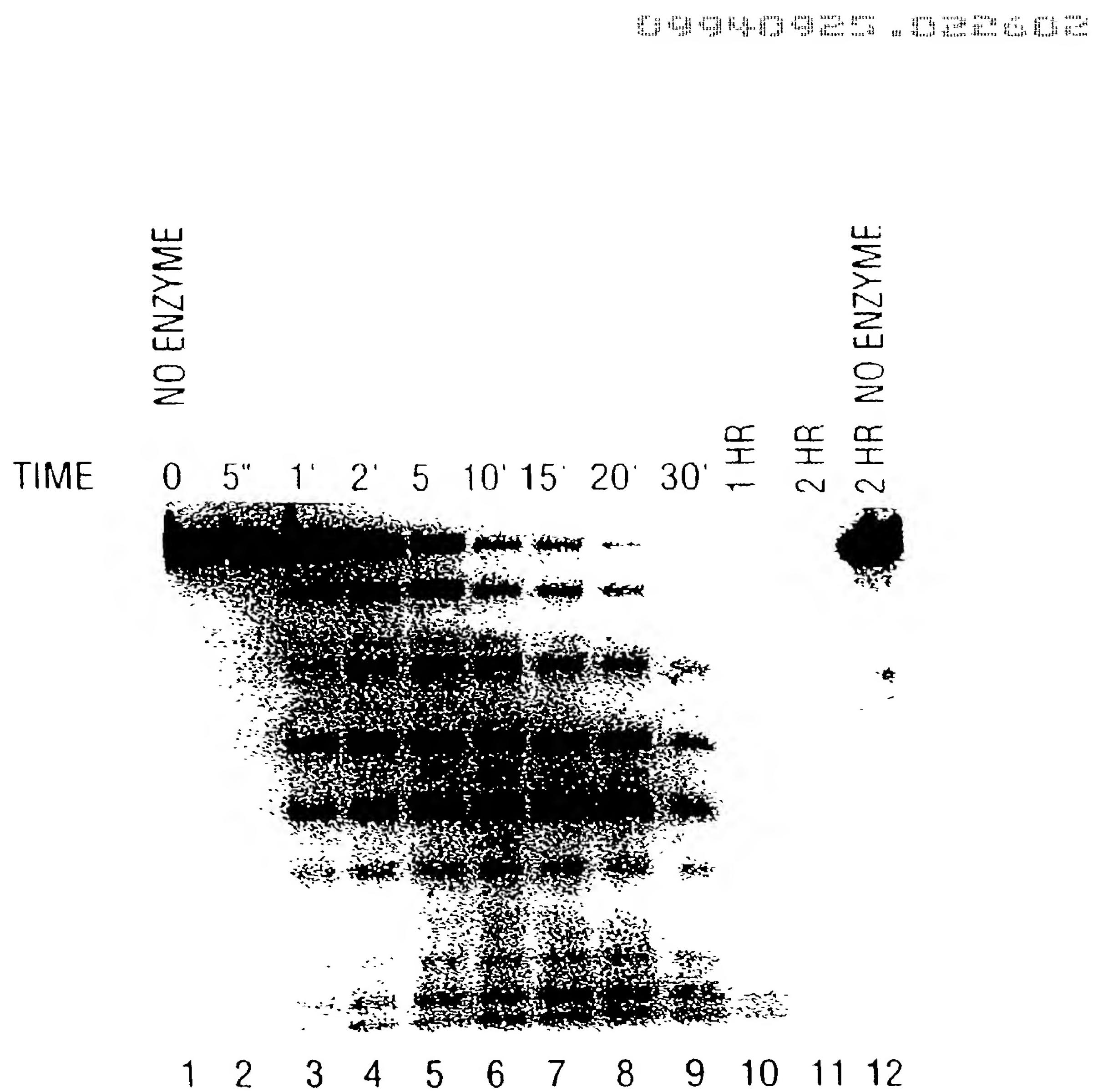


FIG. 60

20 40 60 40 20 20 20 20 20

20 20 20 20 20 20 20 20

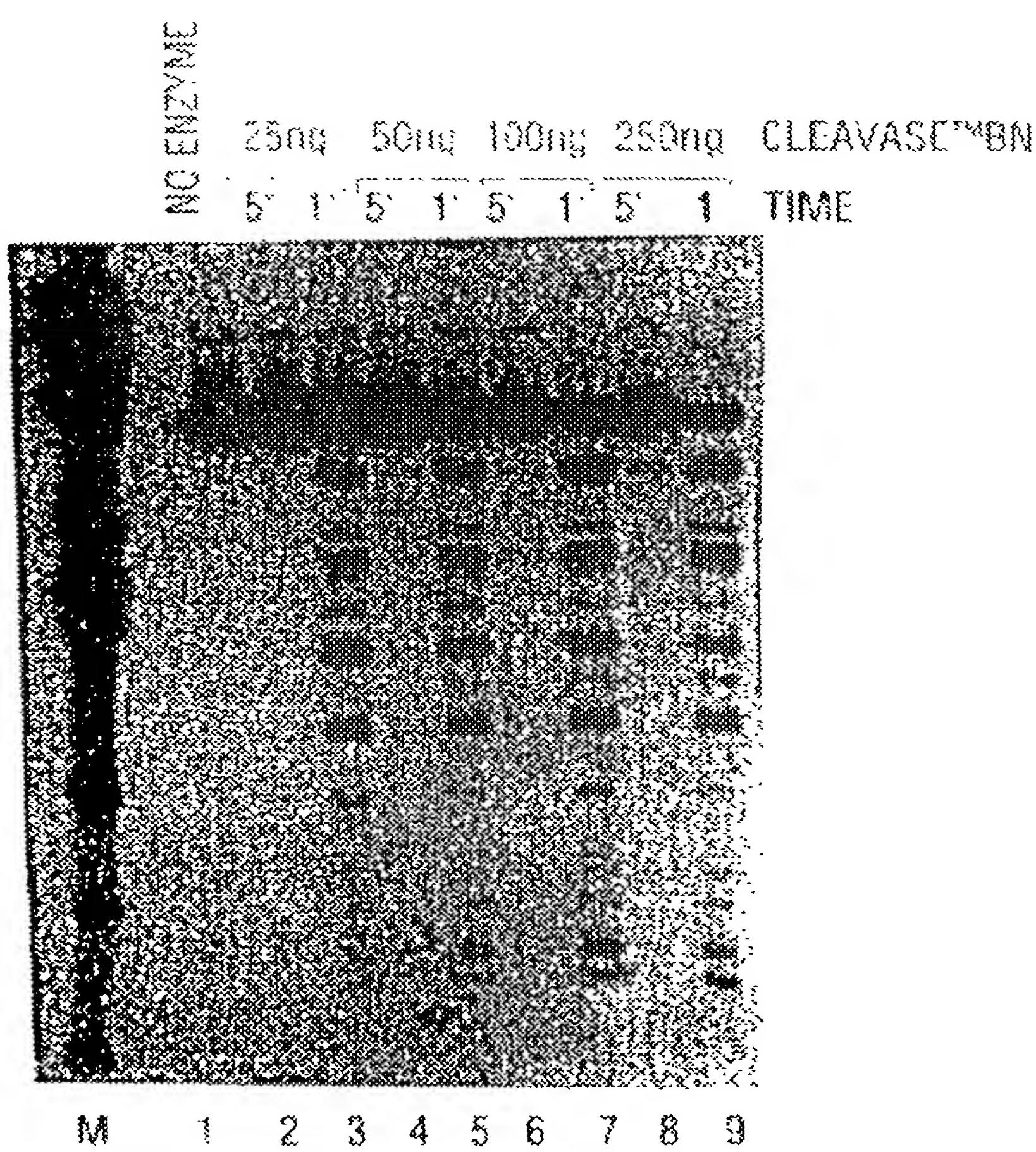


FIG. 61

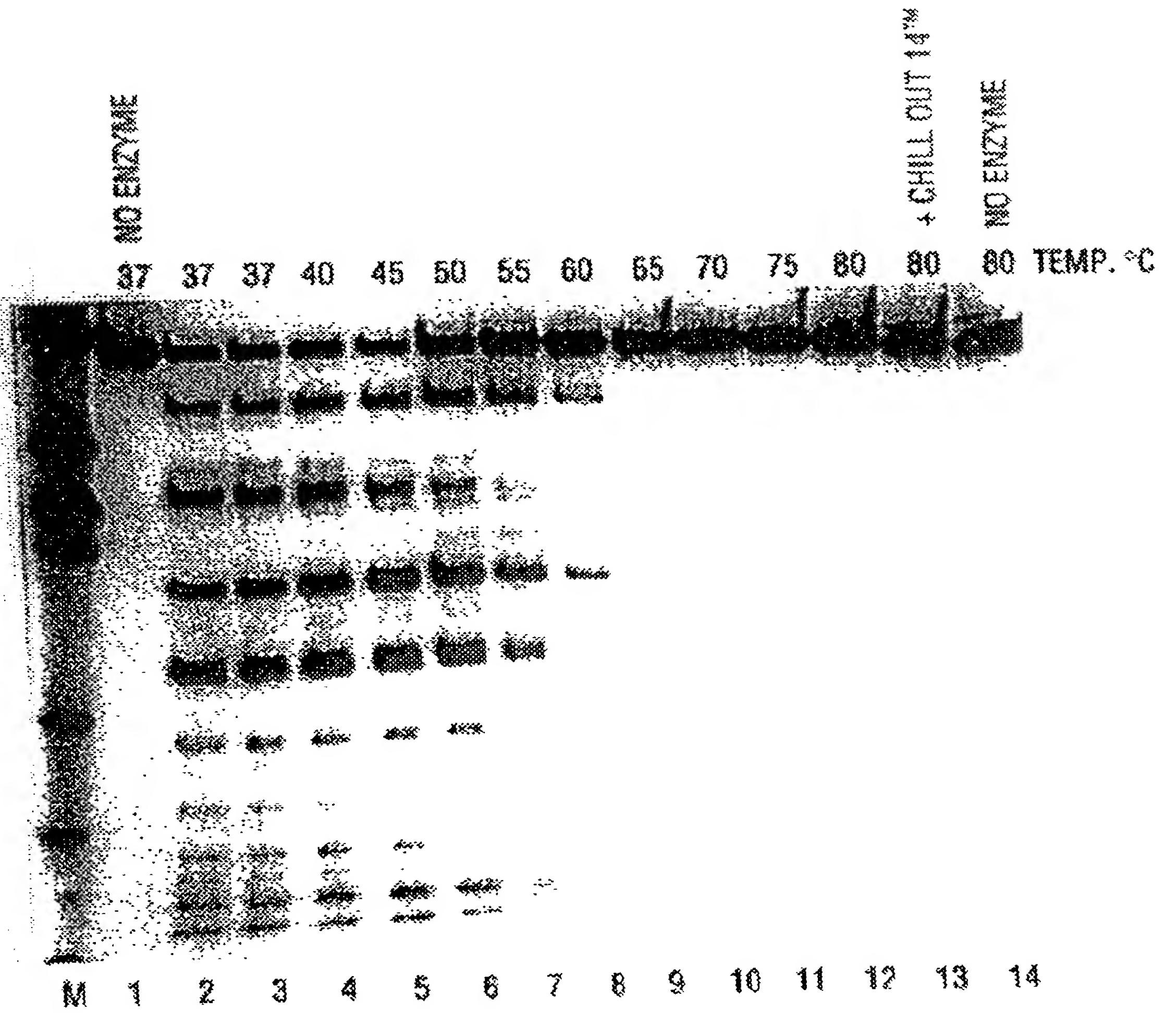


FIG. 62

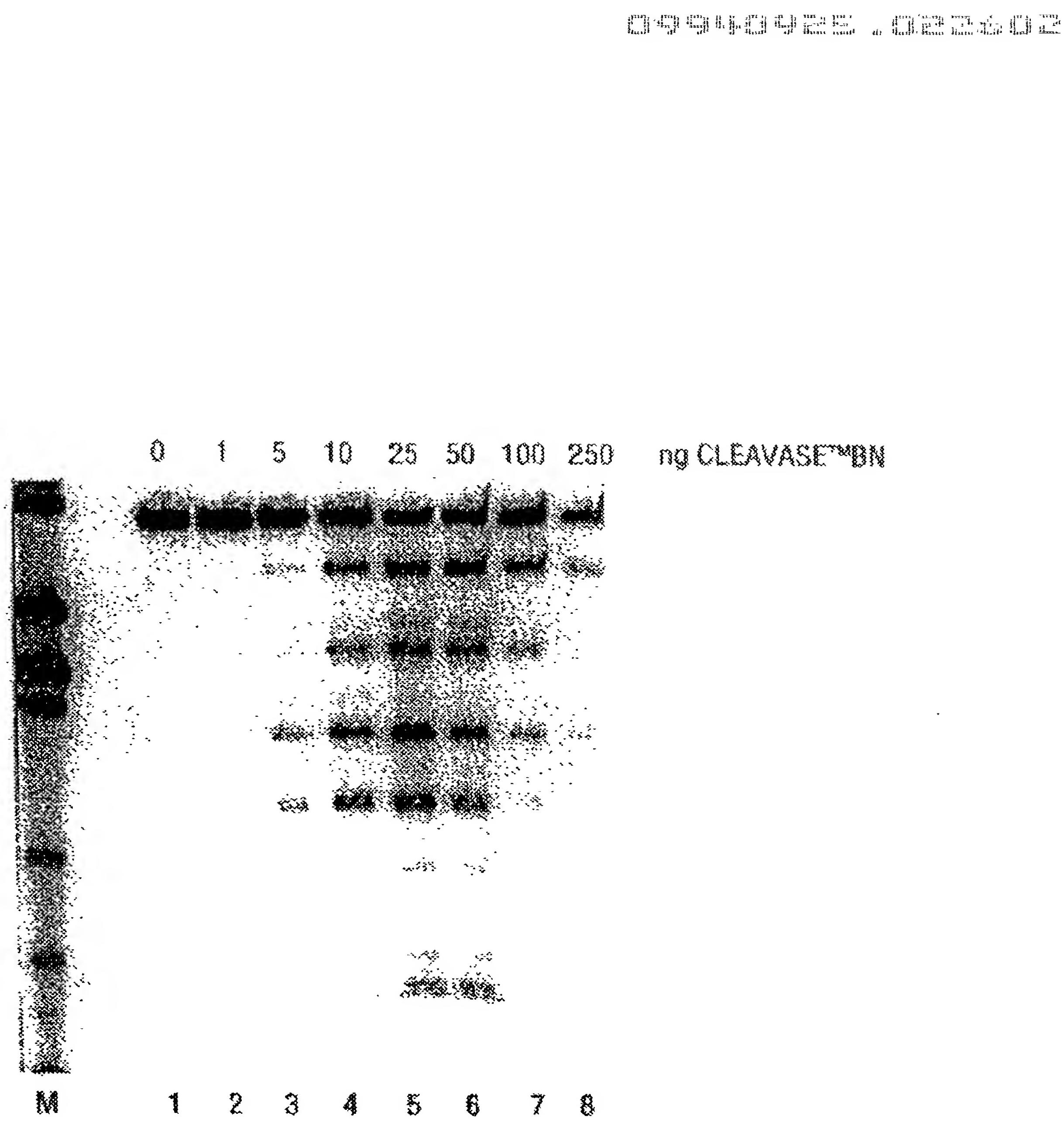


FIG. 63

© 1990 by Marcel Dekker, Inc.

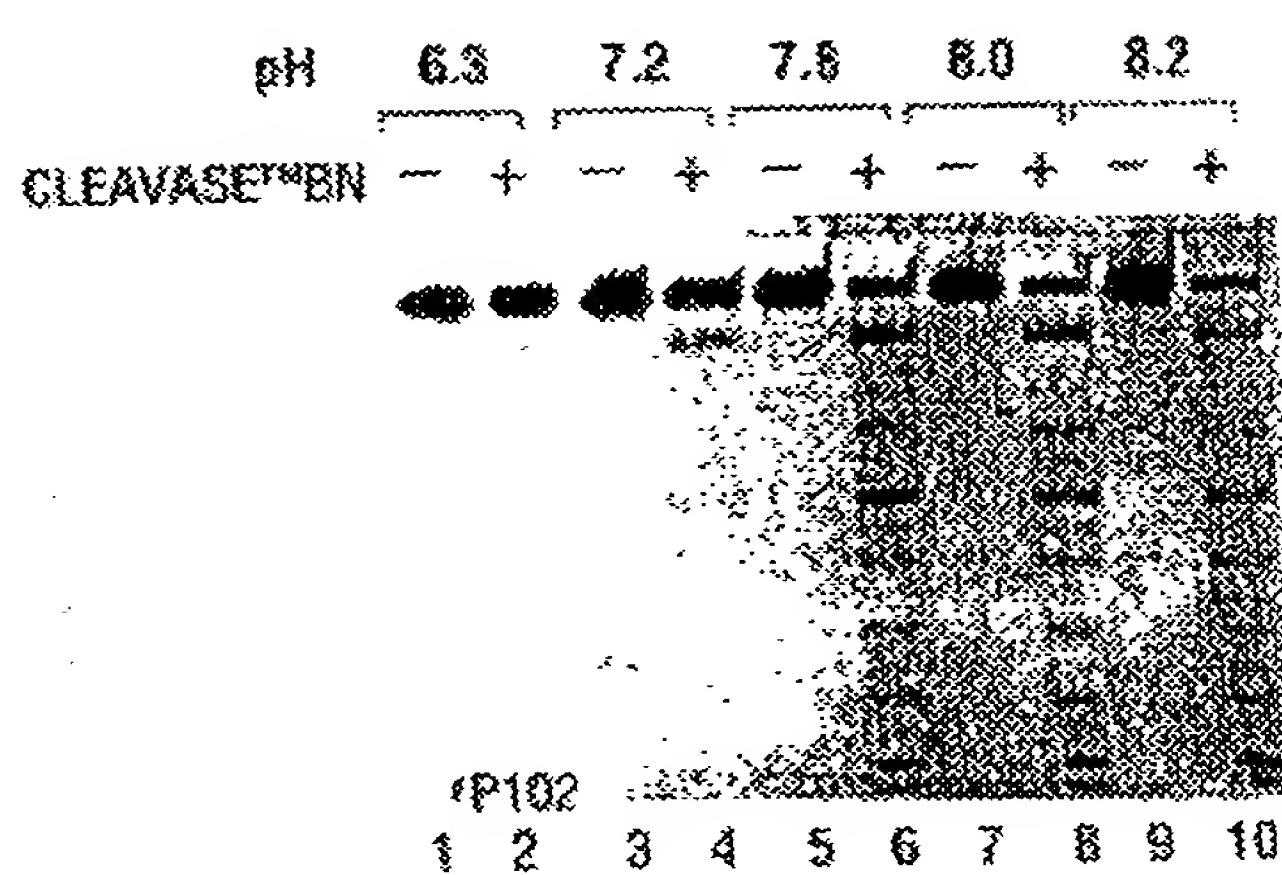


FIG. 64A

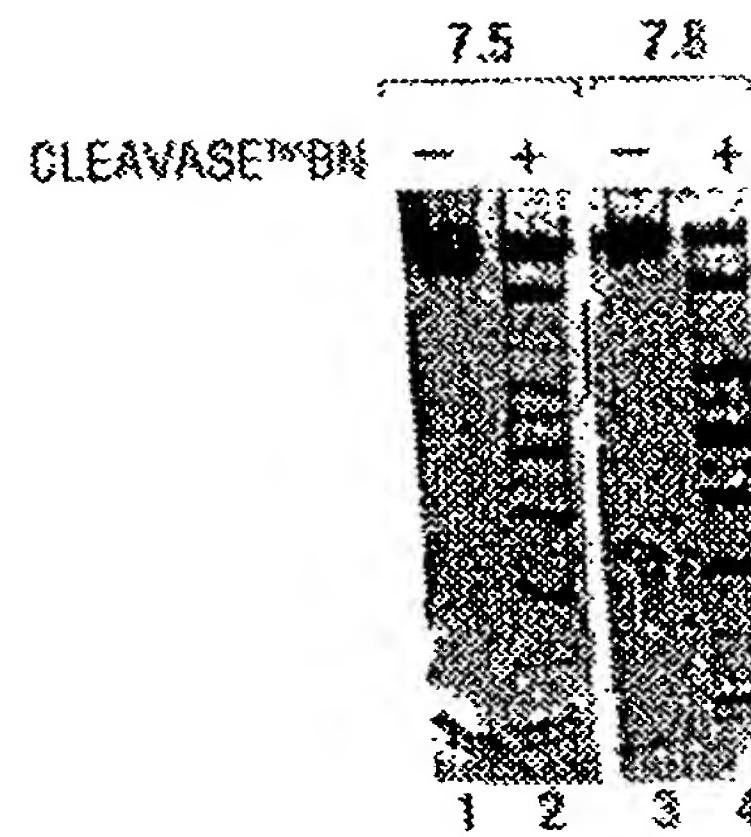


FIG. 64B

0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0

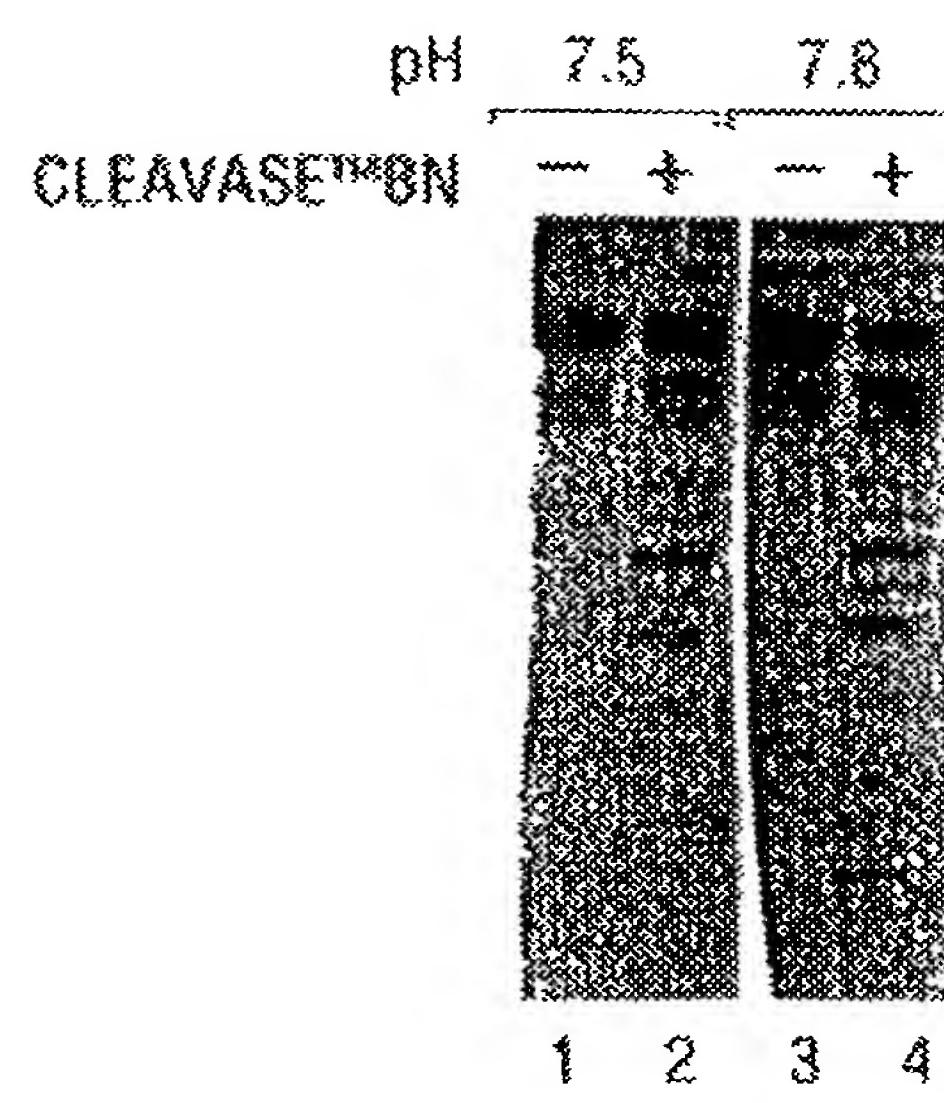
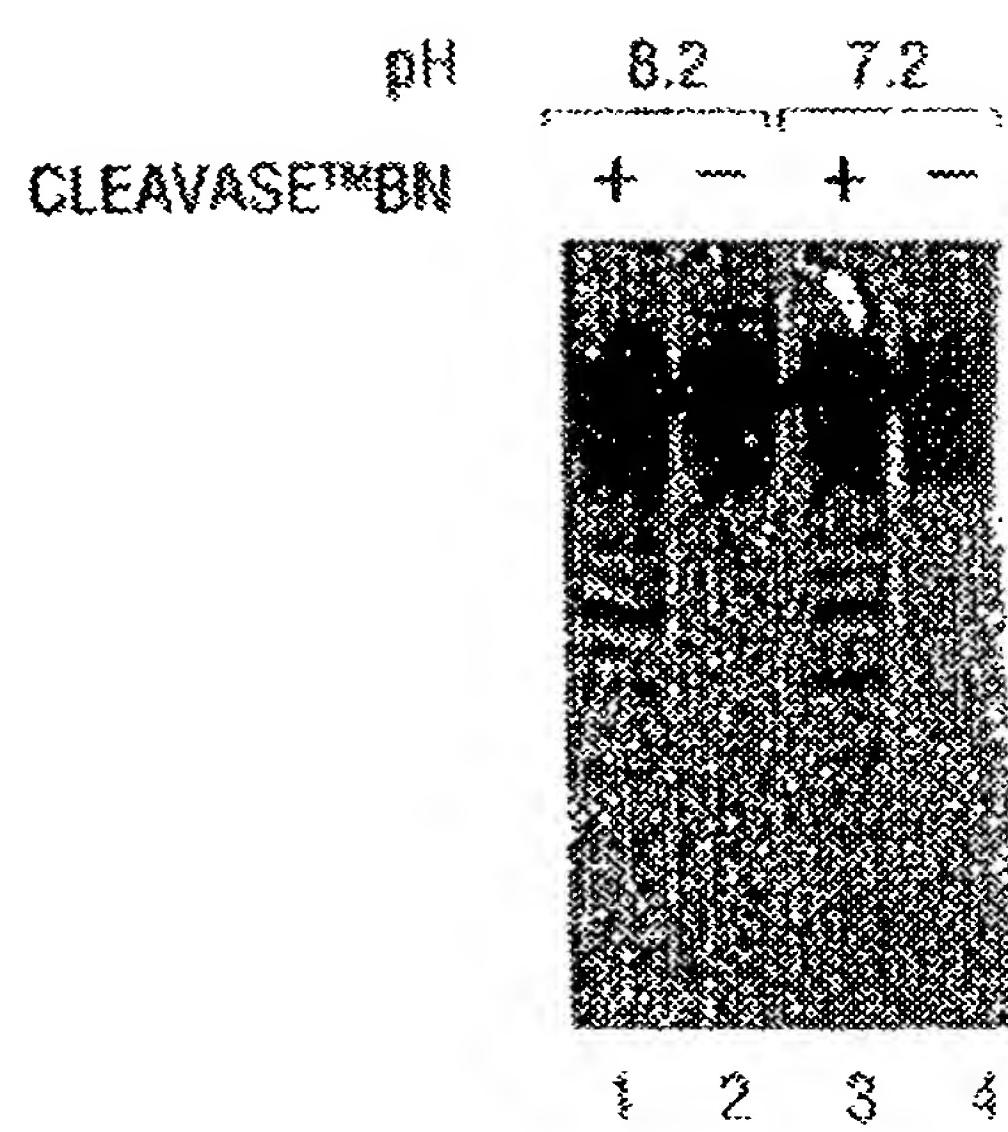


FIG. 65A

FIG. 65B

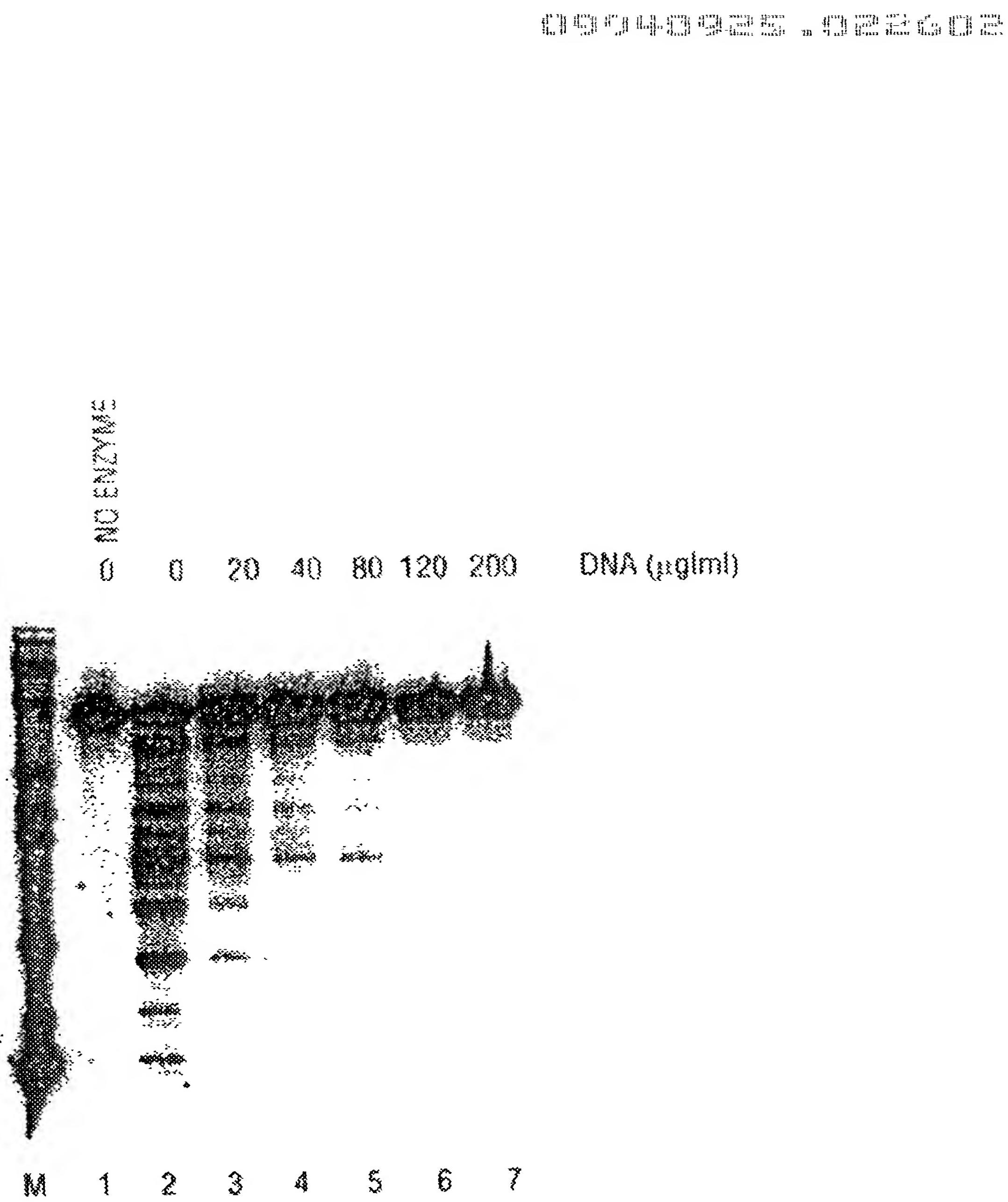


FIG. 66

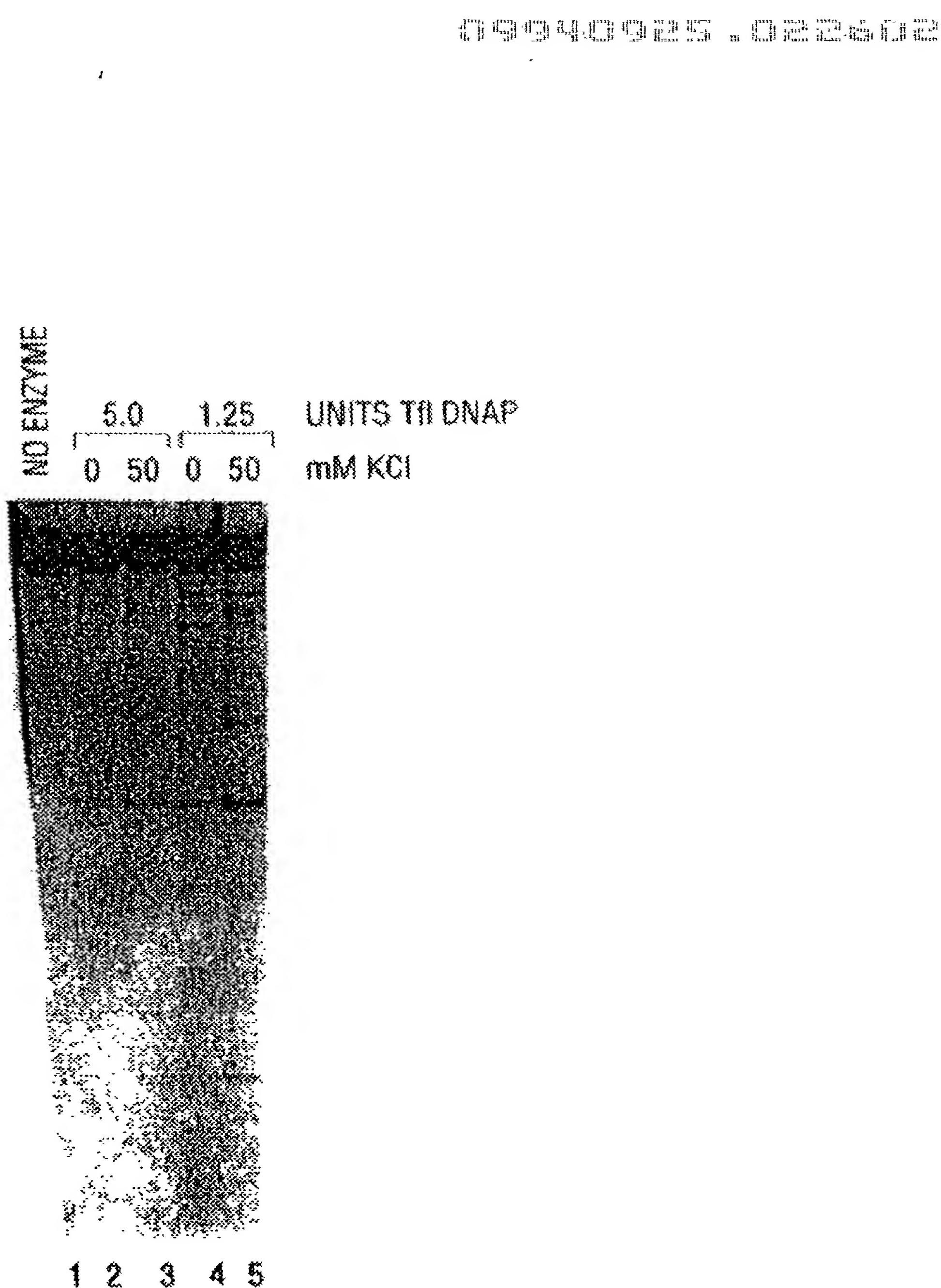


FIG. 67

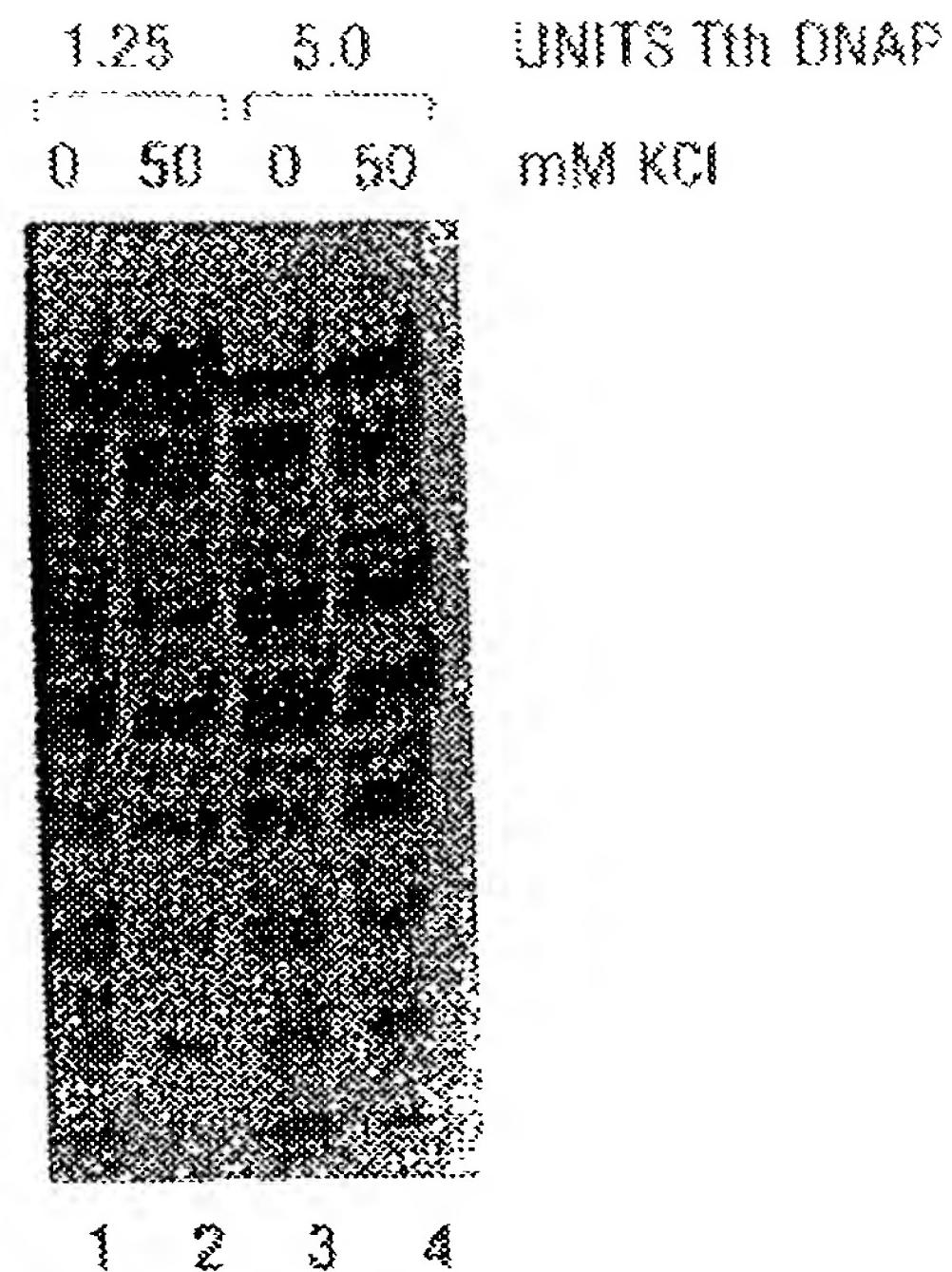


FIG. 68

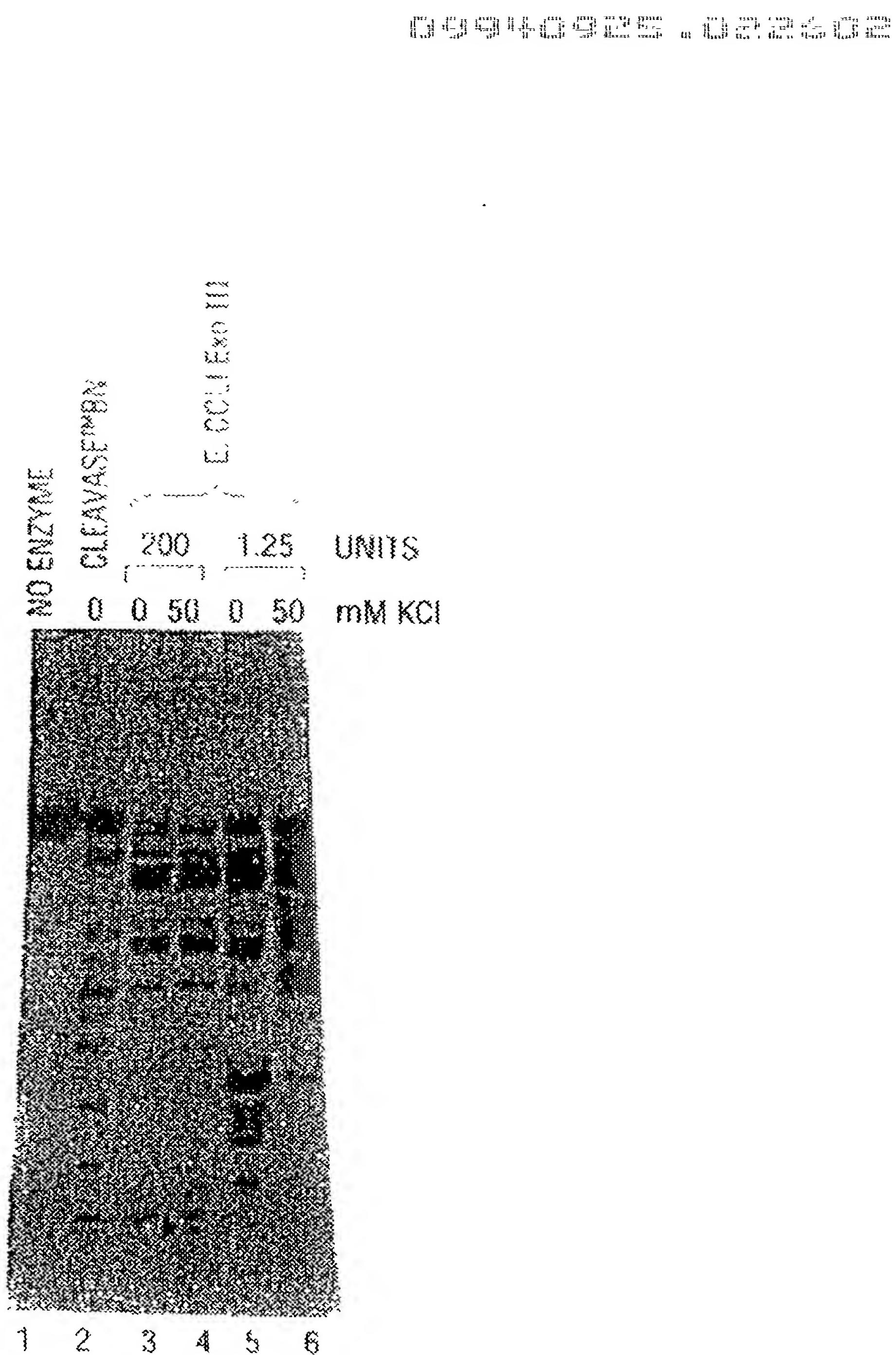


FIG. 69

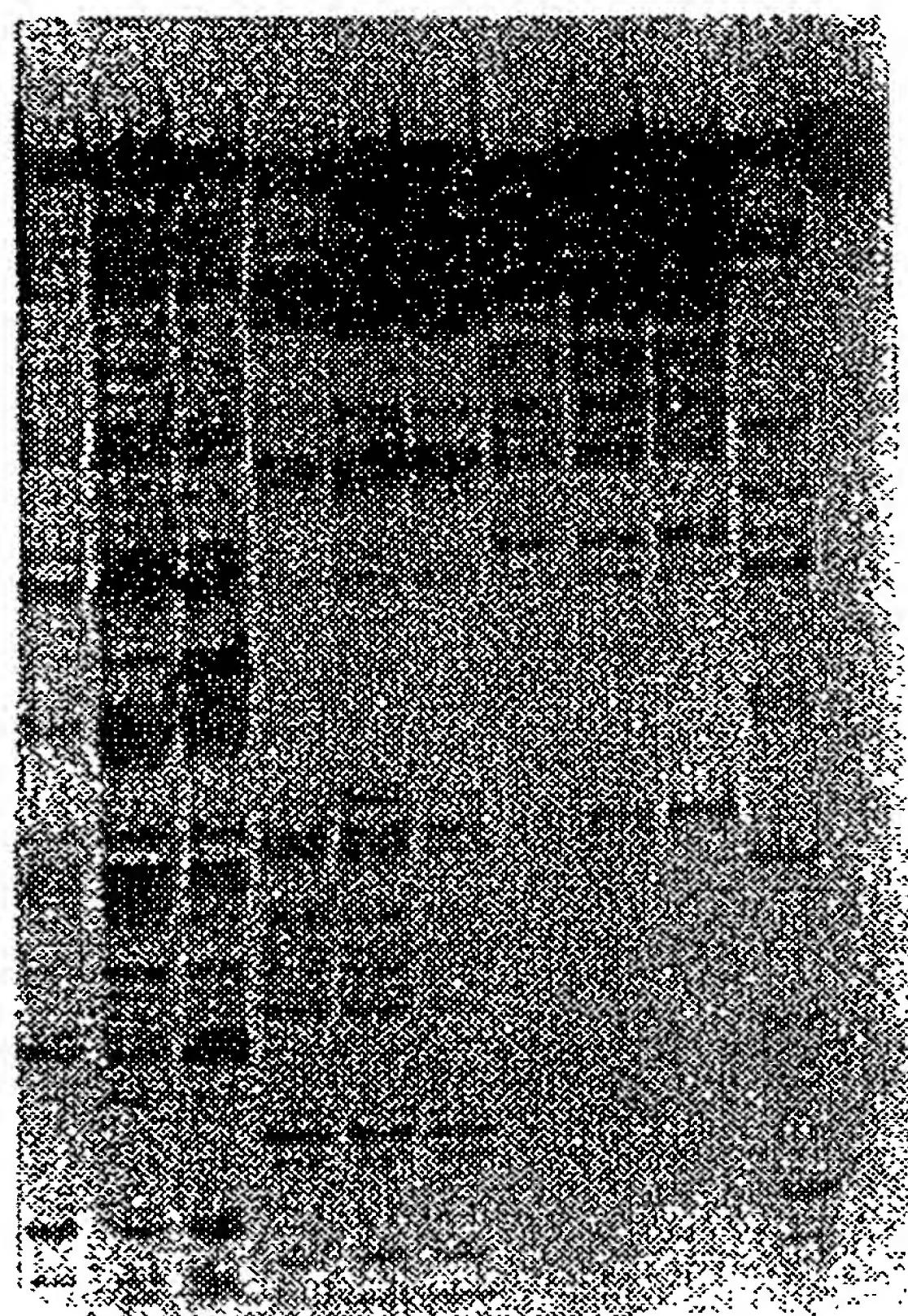
43 43 43 43 43 43 43 43 43 43 43

83

1 C. N. (ex 11)

1% DNAE 0.05M 53 mM

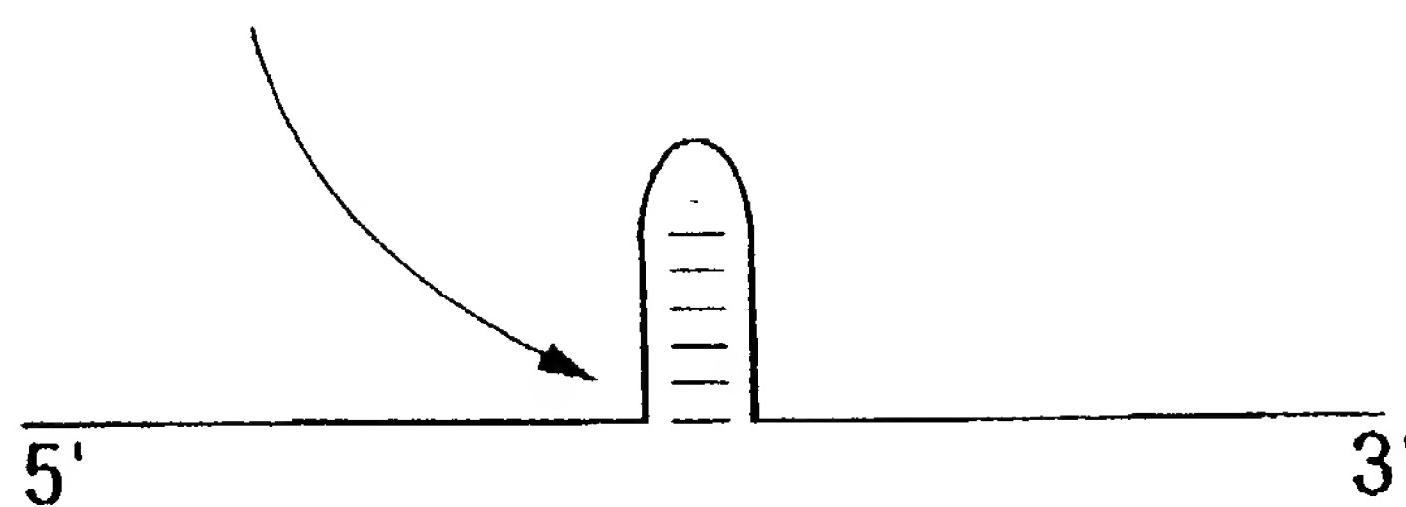
32 32 32 32 32 32



1 2 3 4 5 6 7 8 9 10 11

FIG. 70

5' CLEAVAGE SITE



3' CLEAVAGE SITE

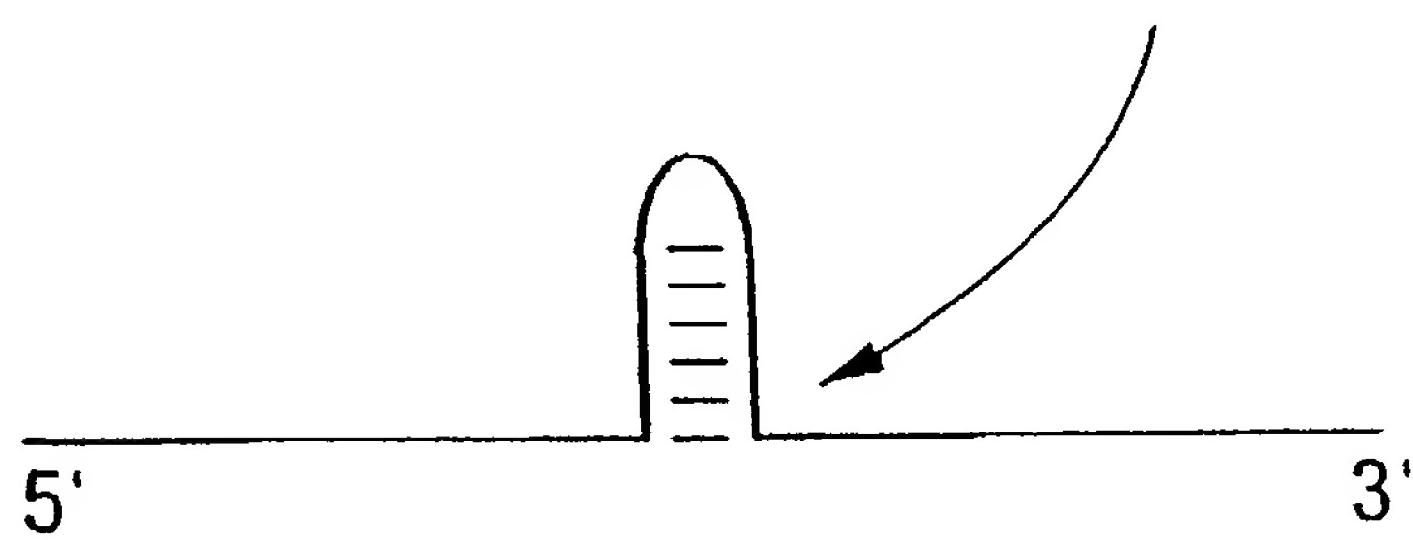


FIG. 71

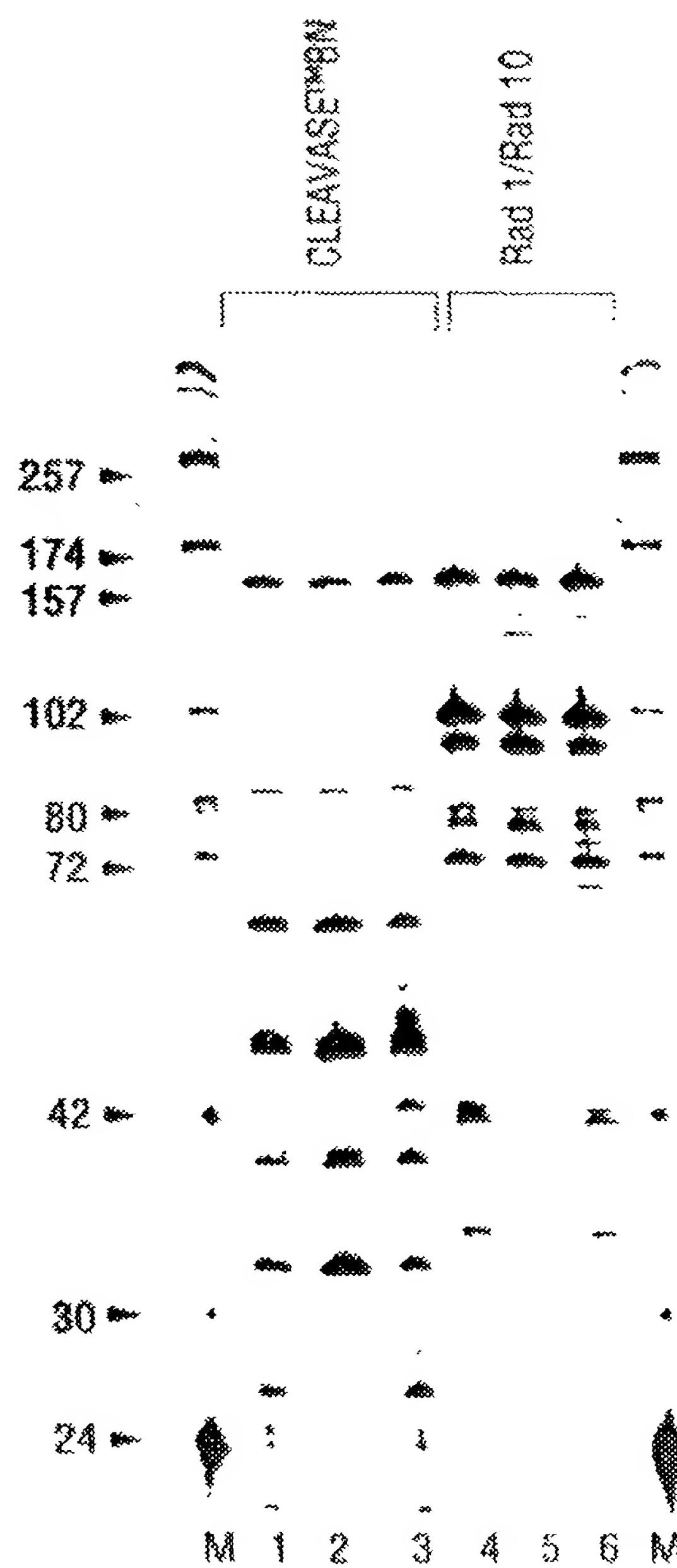


FIG. 72



FIG. 73

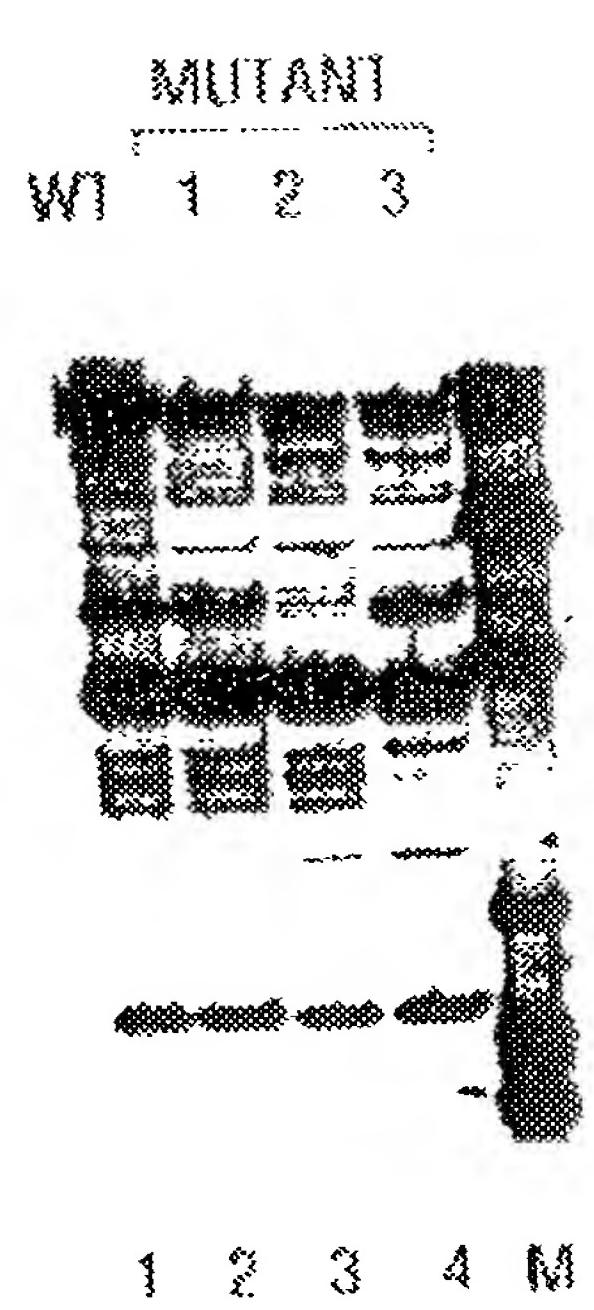


FIG. 74A

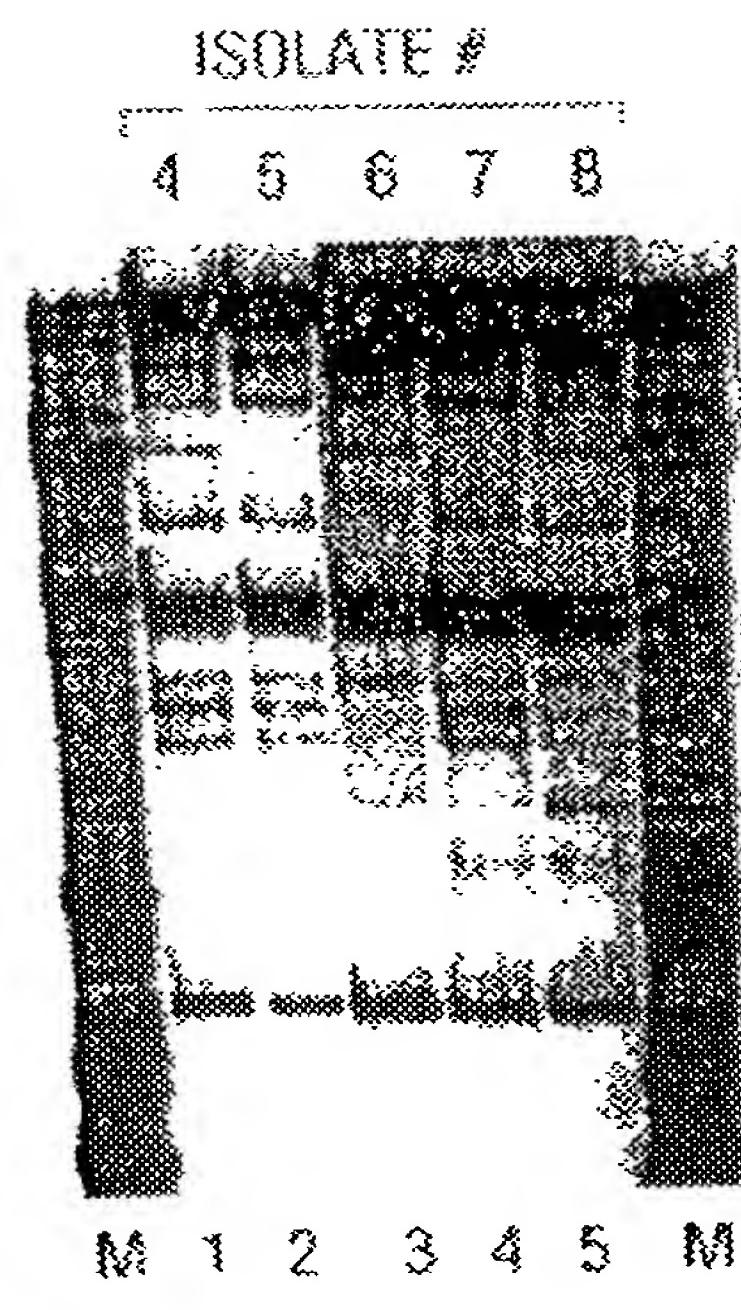


FIG. 74B

100 200 300 400 500 600 700 800 900 1000

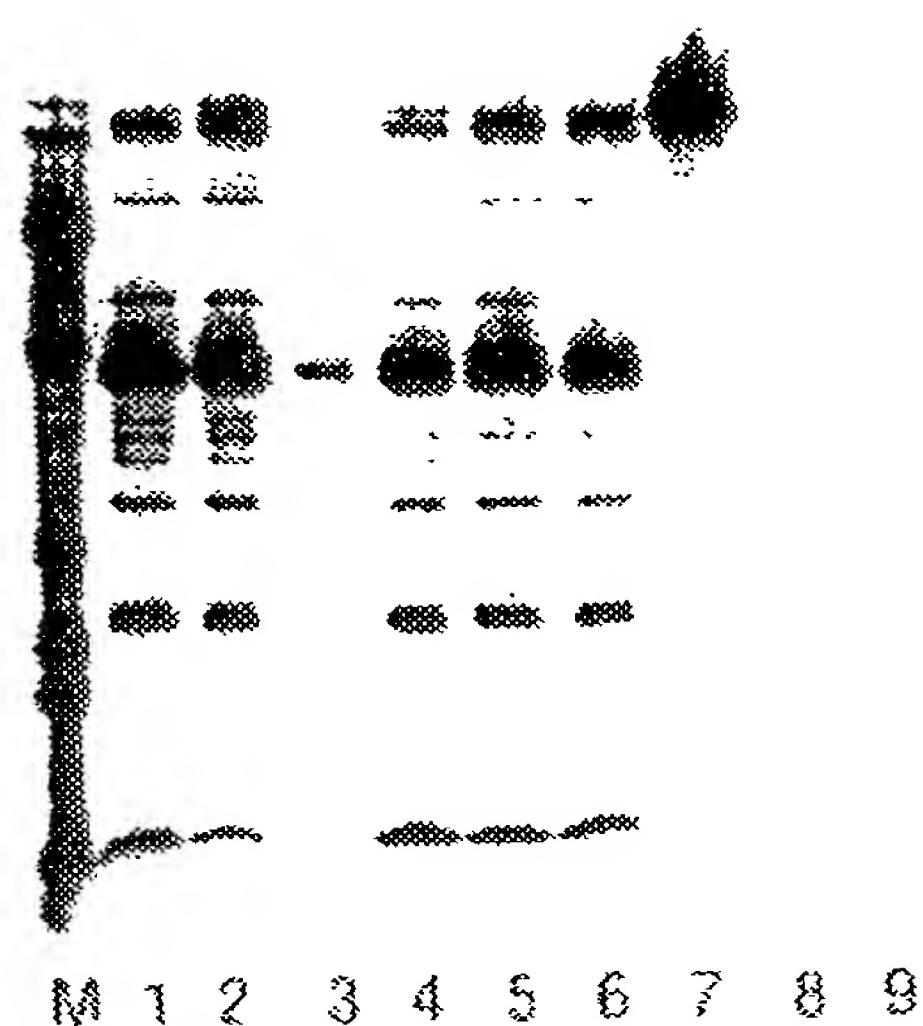


FIG. 75

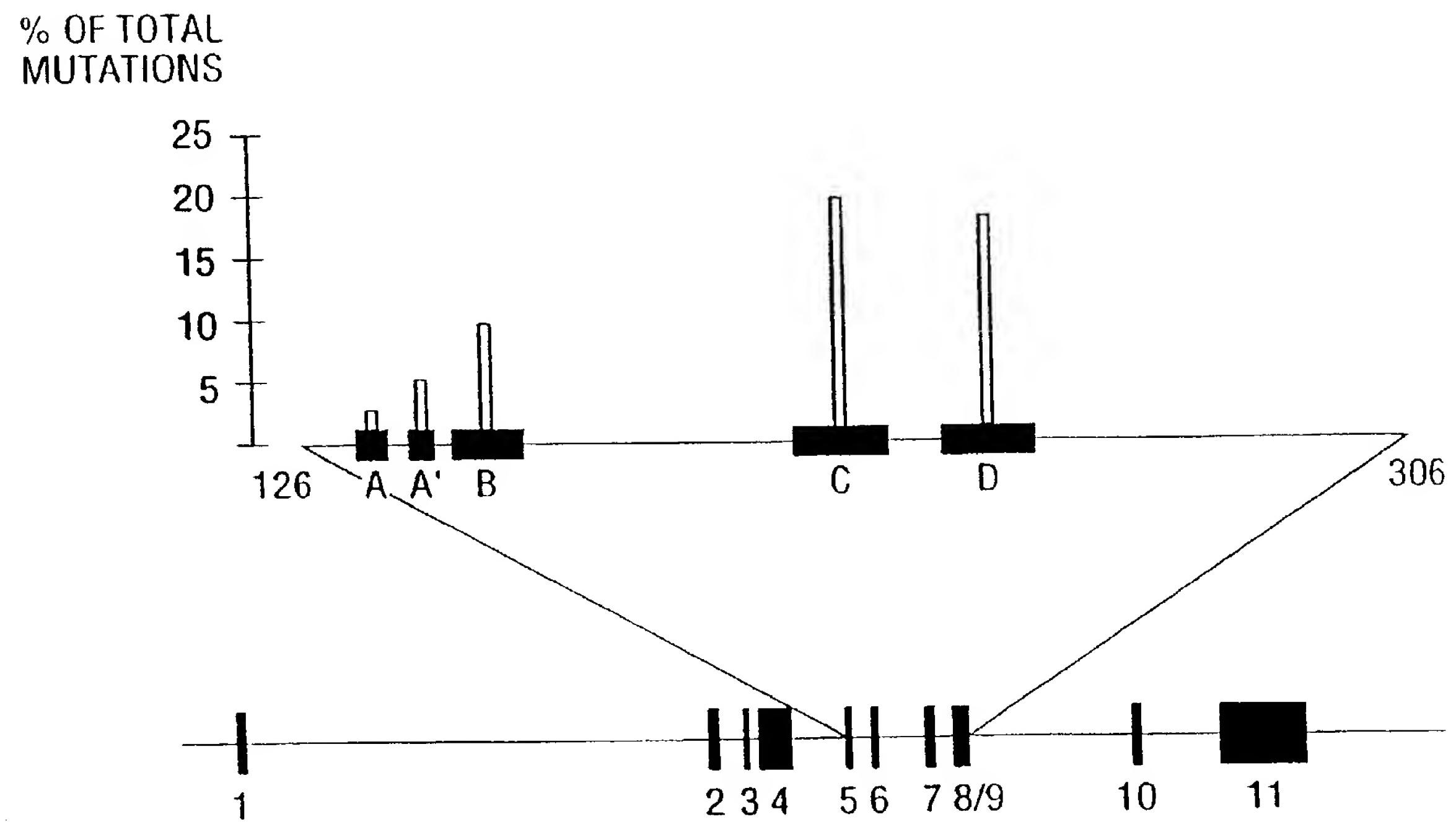


FIG. 76

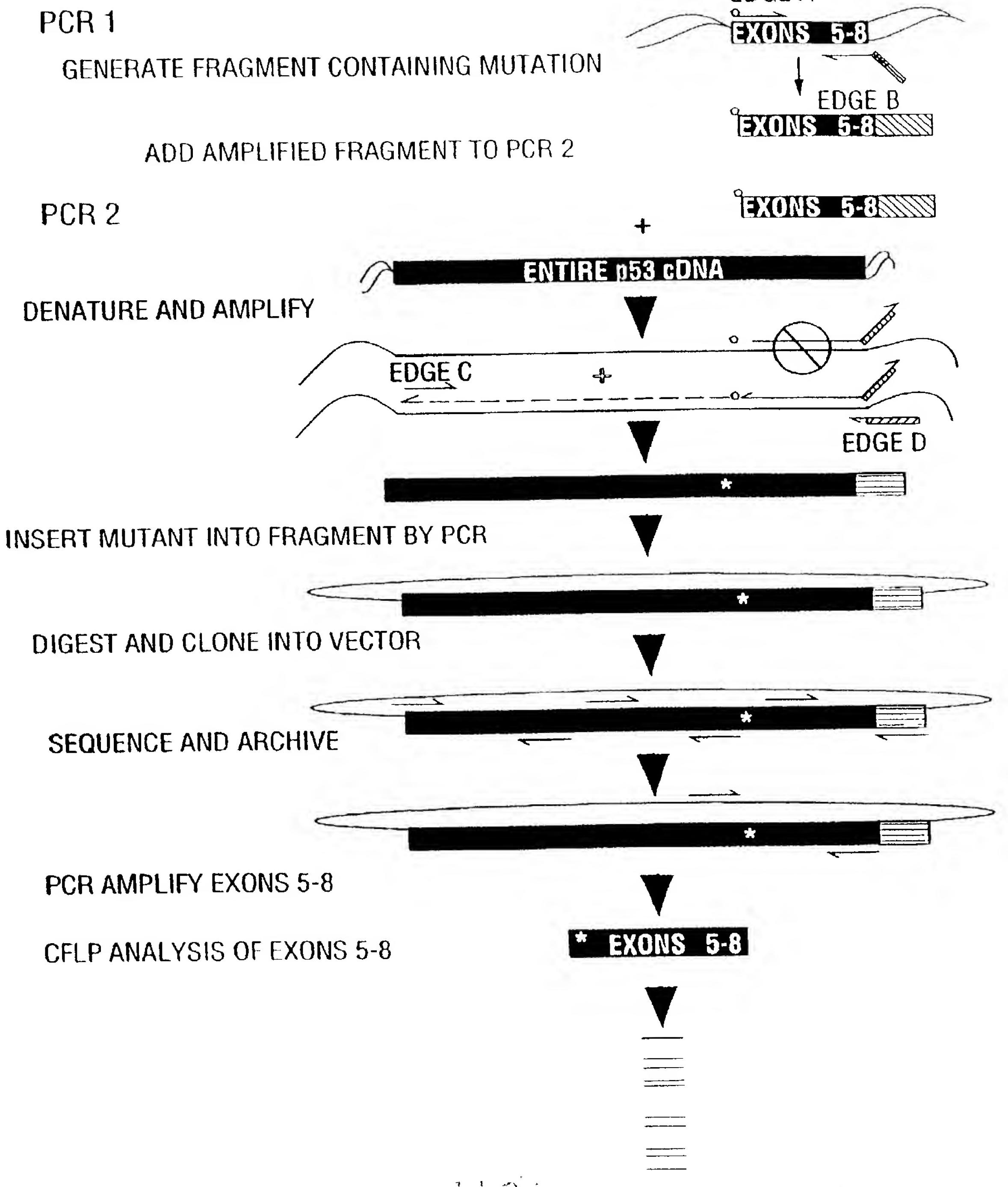


FIG. 77

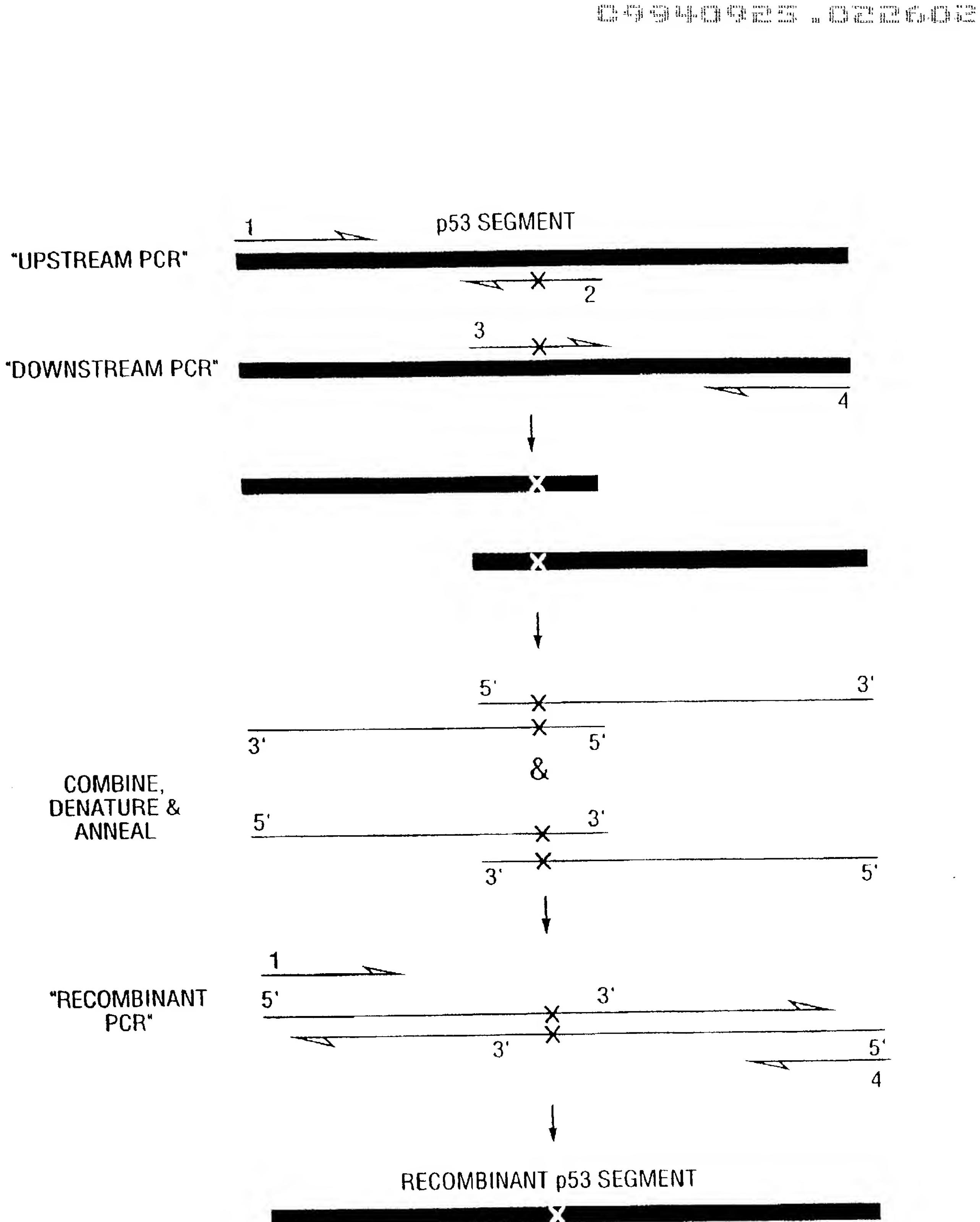


FIG. 78

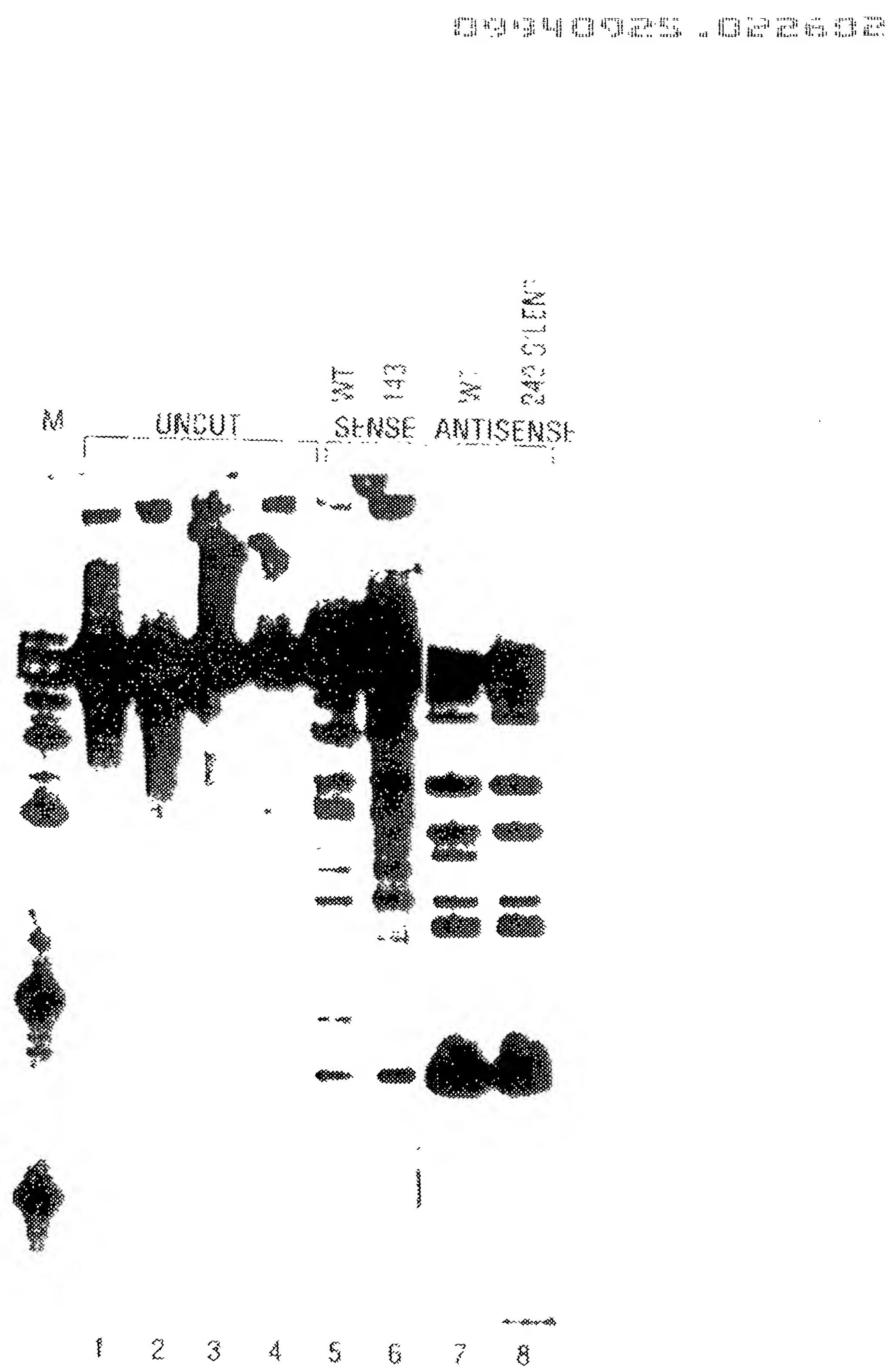


FIG. 79

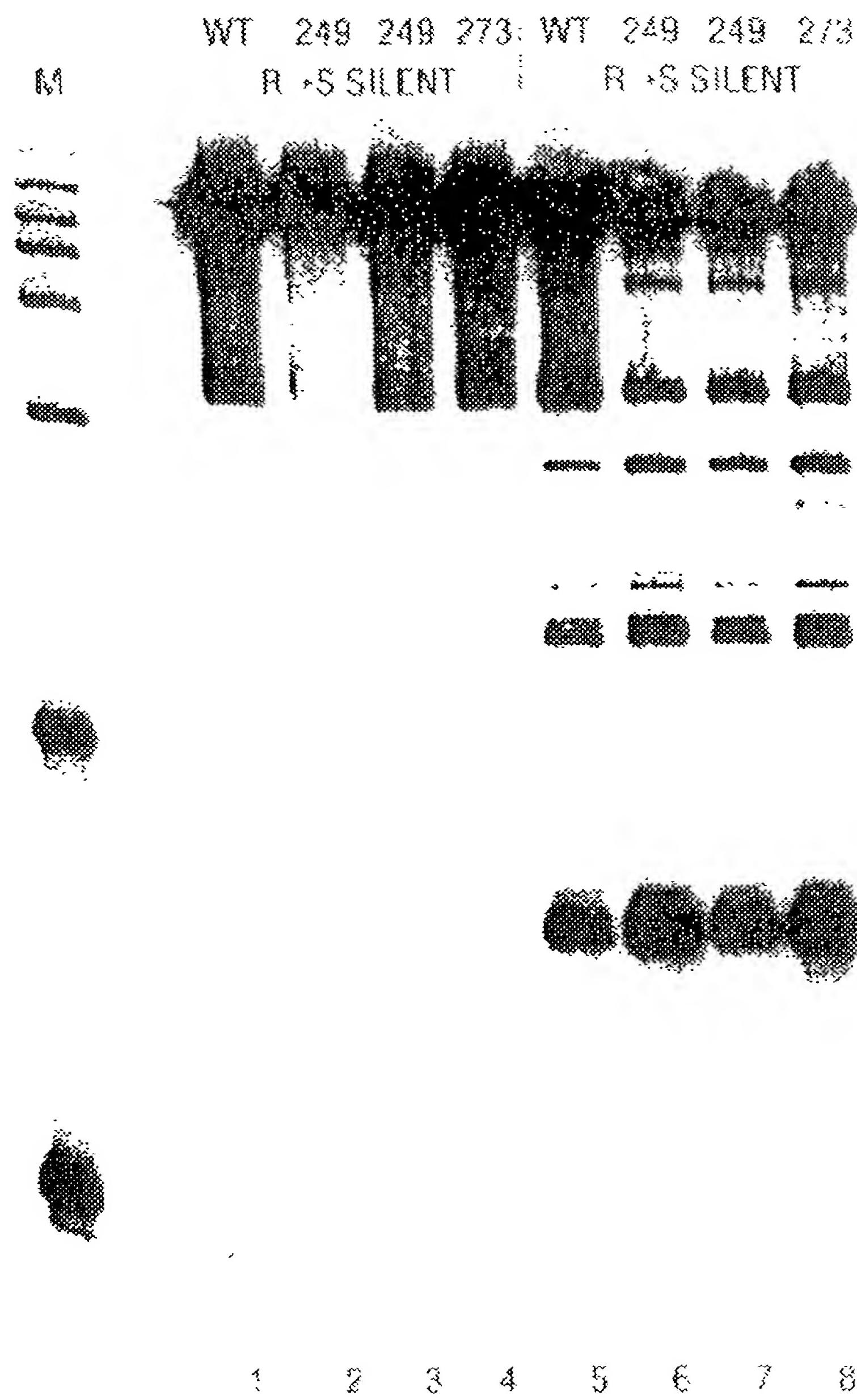


FIG. 80

C₁ C₂ C₃ C₄ C₅ C₆ C₇ C₈ C₉ C₁₀ C₁₁ C₁₂ C₁₃ C₁₄

MIXING PROPORTIONS

	UNCUT	1	1	1	1	0	2	4	8		WILD TYPE
M	WT MUT	0	1	2	9	1	1	1	1	MUTANT	

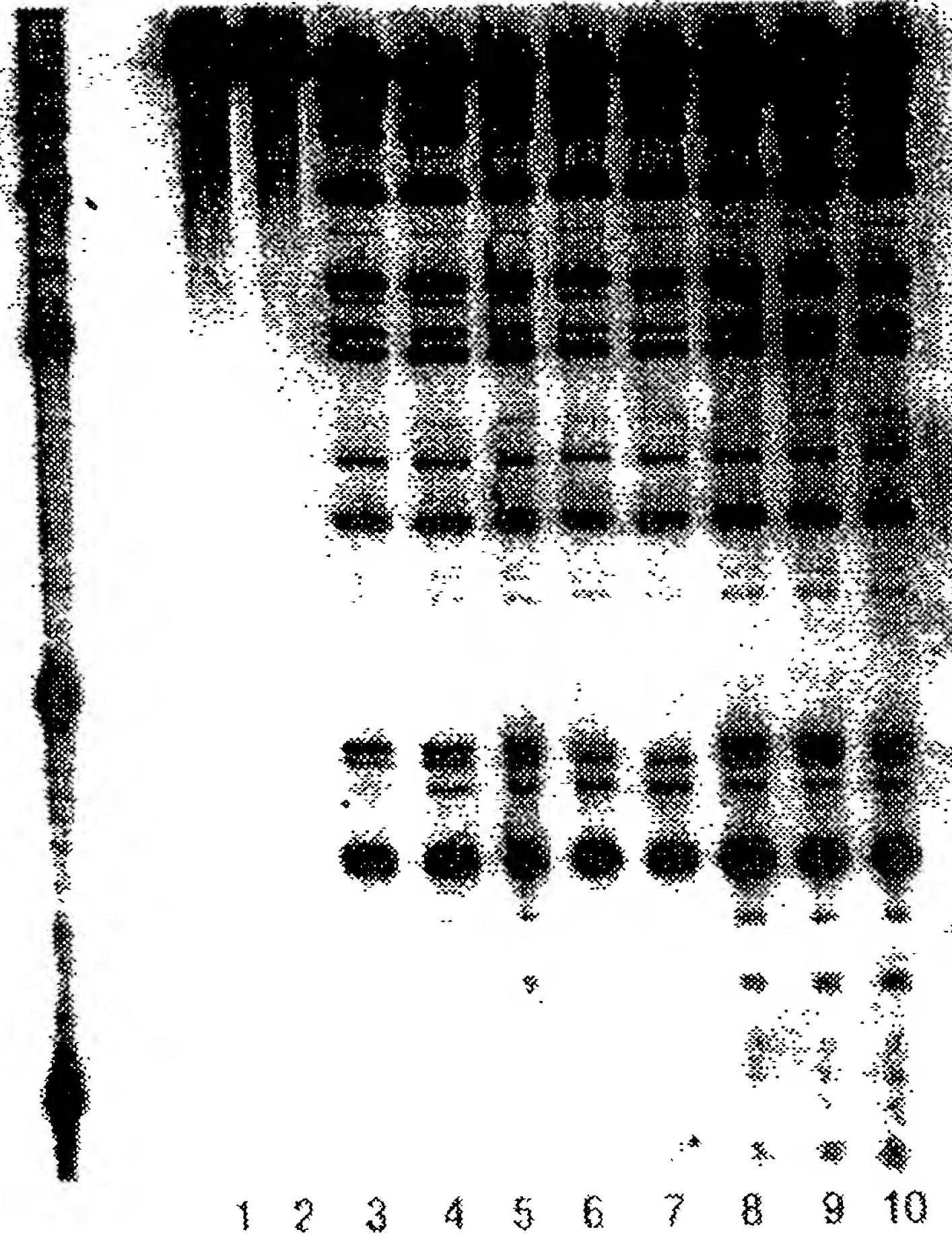


FIG. 81

HCV1.1	(SEQ ID NO:121)	1	CTGTCTTCAC	GCAGAAAGCC	TCTGCCCATG	GGGTTAGTAT	GAGTGTCGTG	50
HCV2.1	(SEQ ID NO:122)		CTGTCTTCAC	GCAGAAAGCC	TCTAGCCATG	GGGTTAGTAT	GAGTGTCGTG	
HCV3.1	(SEQ ID NO:123)		CTGTCTTCAC	GCAGAAAGCC	TCTAGCCATG	GGGTTAGTAT	GAGTGTCGTG	
HCV4.2	(SEQ ID NO:124)		CTGTCTTCAC	GCAGAAAGCC	TCTAGCCATG	GGGTTAGTAT	GAGTGTCGTG	
HCV6.1	(SEQ ID NO:125)		CTGTCTTCAC	GCAGAAAGCC	TCTAGCCATG	GGGTTAGTAT	GAGTGTCGTG	
HCV7.1	(SEQ ID NO:126)		CTGTCTTCAC	GCAGAAAGCC	SCTAGCCATG	GGGTTAGTAC	GAGTGTCGTG	
HCV1.1		51	CAGCCTCCAG	GACCCCCCT	CCCCGGAGAG	CCATAGTGGT	CTGCCGAACC	100
HCV2.1			CAGCCTCCAG	GACCCCCCT	CCCCGGAGAG	CCATAGTGGT	CTGCCGAACC	
HCV3.1			CAGCCTCCAG	G <u>T</u> CCCCCT	CCCCGGAGAG	CCATAGTGGT	CTGCCGAACC	
HCV4.2			CAGCCTCCAG	GACCCCCCT	CCCCGGAGAG	CCATAGTGGT	CTGCCGAACC	
HCV6.1			CAGCCTCCAG	GCCCCCCC	CCCCGGAGAG	CCATAGTGGT	CTGCCGAACC	
HCV7.1			CAGCCTCCAG	GACCCCCCT	CCCCGGAGAG	CCATAGTGGT	CTGCCGAACC	
HCV1.1		101	GGTAGTACA	CCGGAAATTGC	CAGGACGGACC	GGGTCCCTTC	TTGGAT- <u>AAA</u>	150
HCV2.1			GGTAGTACA	CCGGAAATTGC	CAGGACGGACC	GGGTCCCTTC	TTGGAT-CAA	
HCV3.1			GGTAGTACA	CCGGAAATTGC	CAGGACGGACC	GGGTCCCTTC	TTGGAT-CAA	
HCV4.2			GGTAGTACA	CCGGAAATTGC	CAGGACGGACC	GGGTCCCTTC	<u>GTGGATGTAA</u>	
HCV6.1			GGTAGTACA	CCGGAAATTGC	C <u>GGGAAGACT</u>	GGGTCCCTTC	TTGGAT- <u>AAA</u>	
HCV7.1			GGTAGTACA	CCGGAAATTGC	<u>TGGGGTGACC</u>	GGGTCCCTTC	TTGGAG-CAA	

FIG. 82A

151	HCV1.1 HCV2.1 HCV3.1 HCV4.2 HCV6.1 HCV7.1	CCCCGCTCAAT CCCCGCTCAAT CCCCGCTCAAT CCCCACTCTAT CCCCGCTCAAT ACCCAGAAAT	GGTTCGGAAA GGCCTTGTGG GGTTCGGAAA GGCCTTGTGG GGTTCGGAAA GGCCTTGTGG	TACTGCCCTGA TACTGCCCTGA TACTGCCCTGA TACTGCCCTGA TACTGCCCTGA TACTGCCCTGA	250
201	HCV1.1 HCV2.1 HCV3.1 HCV4.2 HCV6.1 HCV7.1	AGTAGTGTTC AGTAGTGTTC AGTAGTGTTC AGTAGTGTTC AGTAGTGTTC AGTAGTGTTC	GGTTCGGAAA GGCCTTGTGG GGTTCGGAAA GGCCTTGTGG GGTTCGGAAA GGCCTTGTGG	TACTGCCCTGA TACTGCCCTGA TACTGCCCTGA TACTGCCCTGA TACTGCCCTGA TACTGCCCTGA	282
251	HCV1.1 HCV2.1 HCV3.1 HCV4.2 HCV6.1 HCV7.1	GCGAGTCCC GCGAGTCCC GCGAGTCCC GCGAGTCCC GCGAGTCCC GCGAGTCCC	CCTAGACCGT CCTAGACCGT CCTAGACCGT CCTAGACCGT CCTAGACCGT CCTAGACCGT	GC 282	GC 282

FIG. 82B

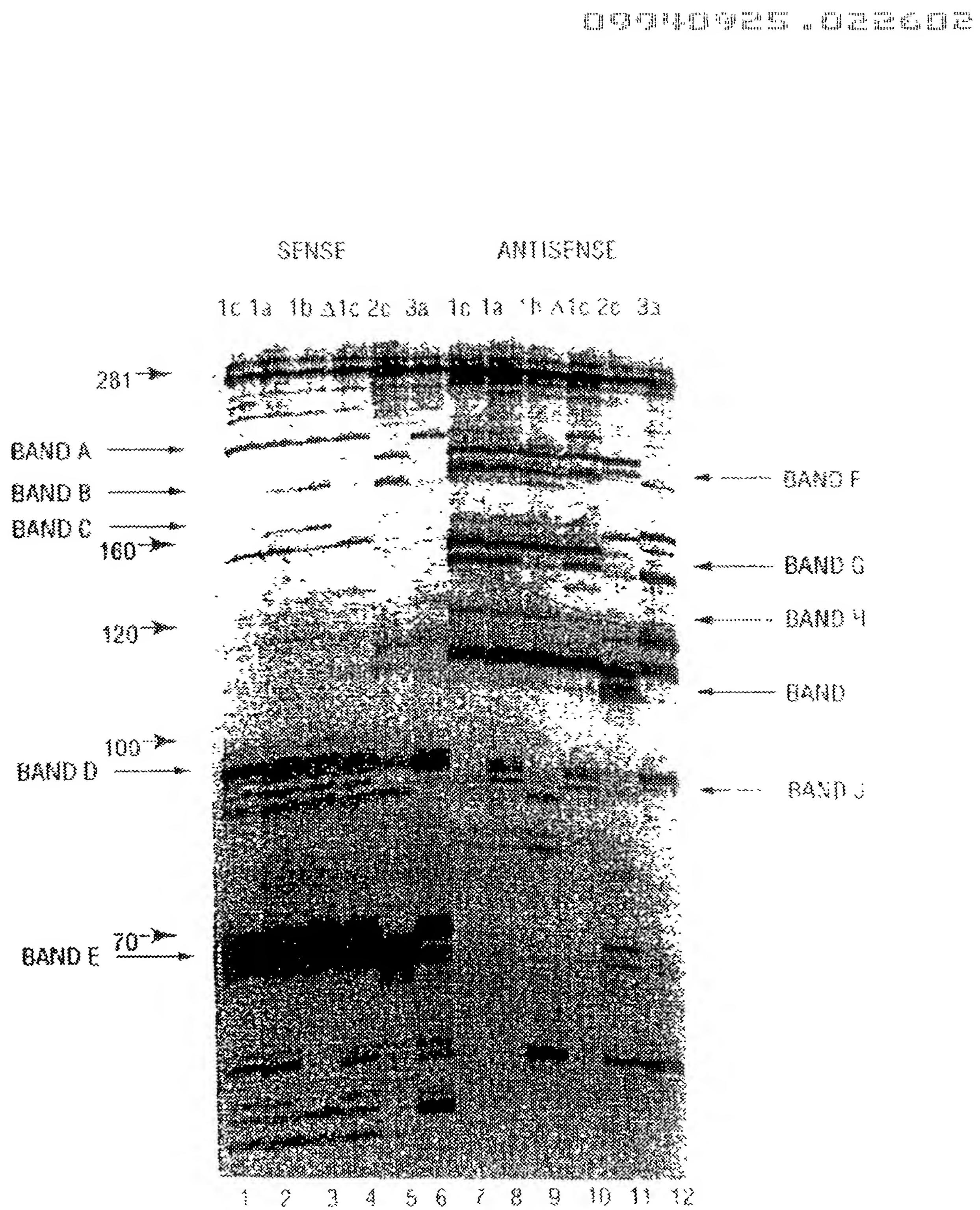


FIG. 83

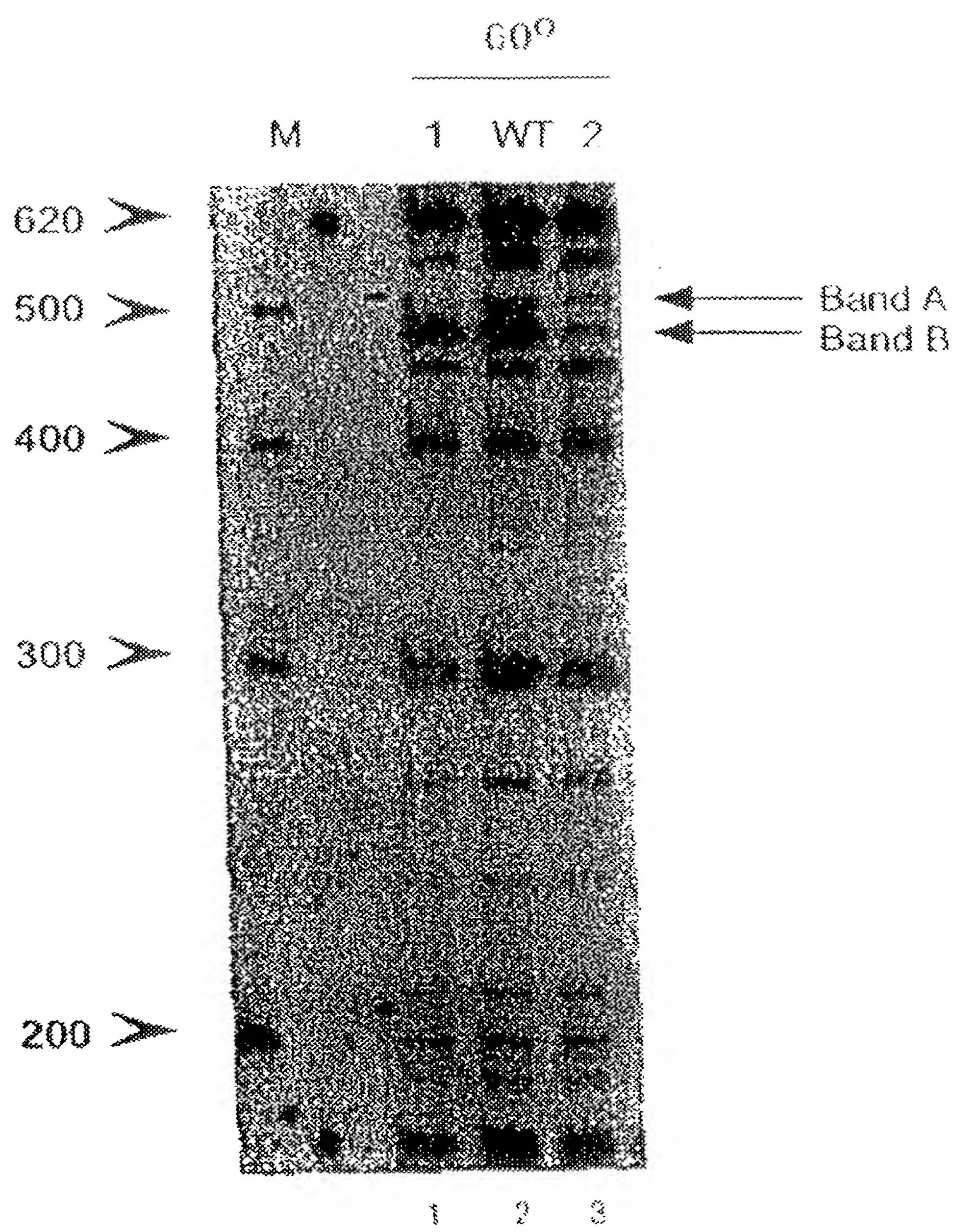


FIG. 84

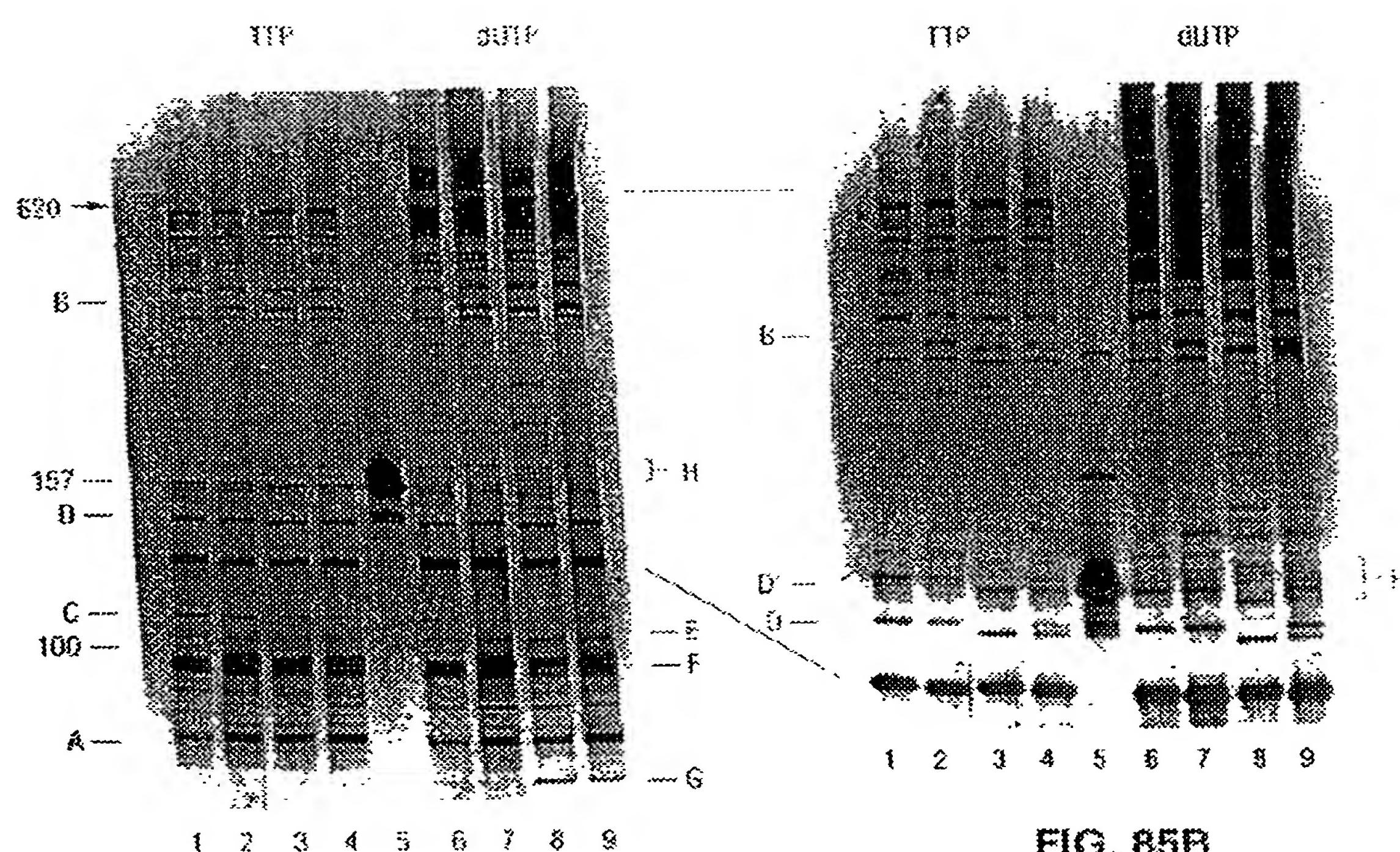


FIG. 85A

420 430 440 450 460 470 480 490 500 510 520 530 540

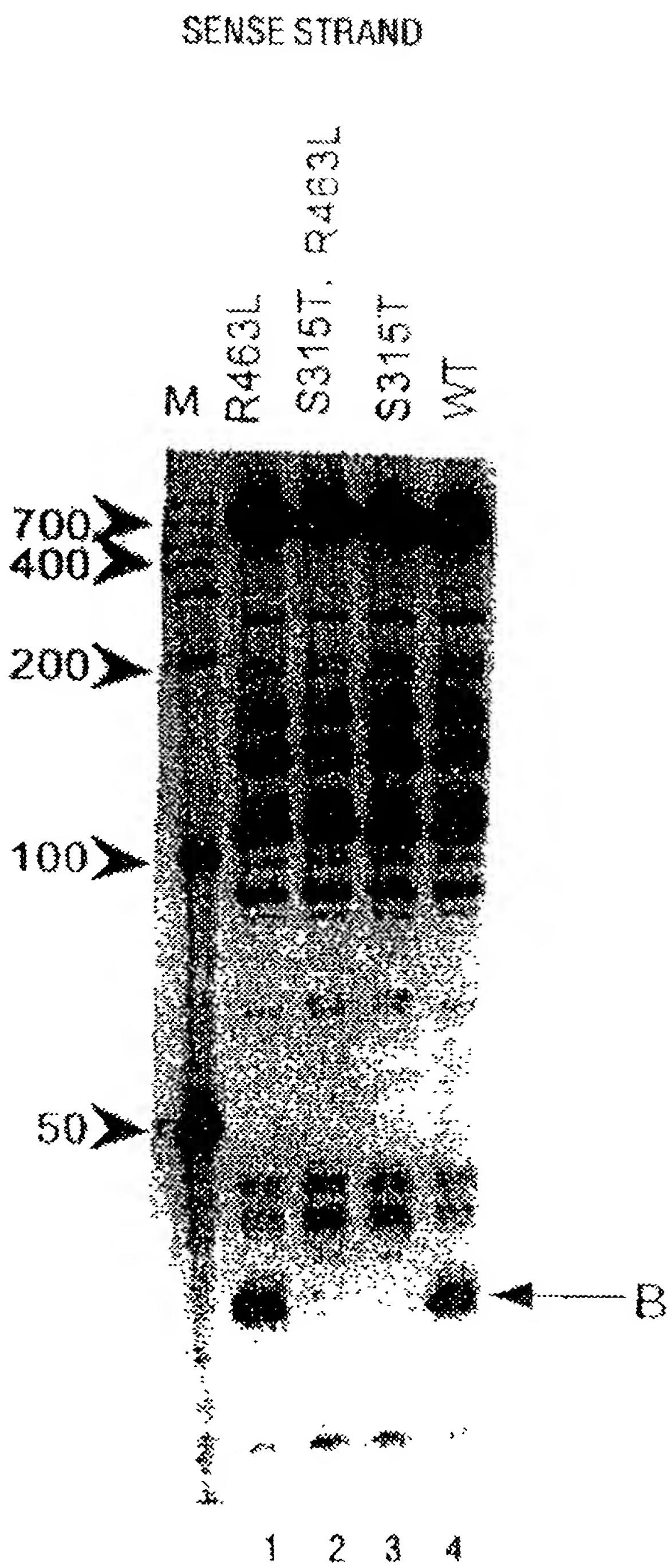


FIG. 86

ANTISENSE STRAND

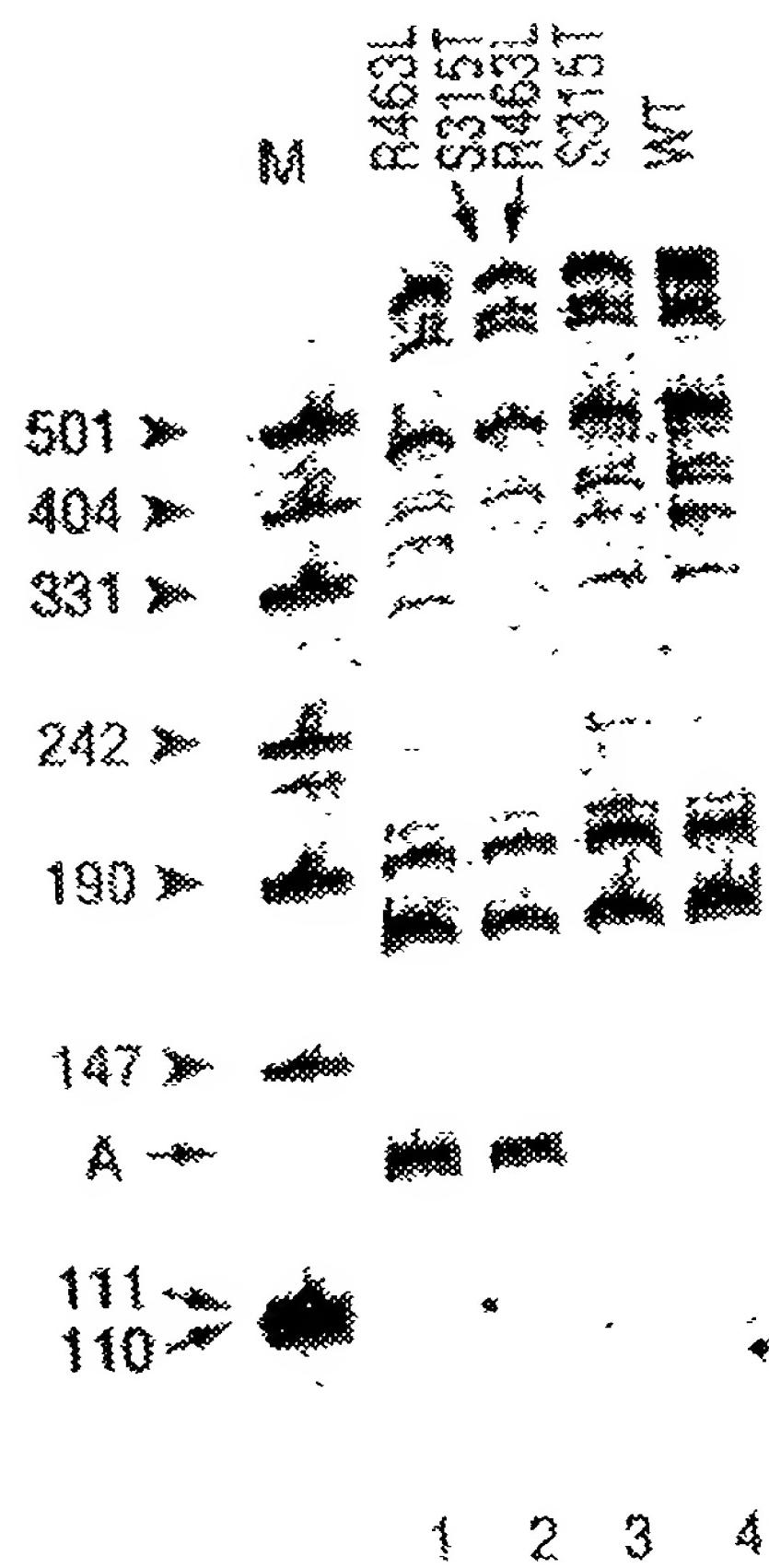


FIG. 87

10	AGA	GTTTGATCCT	<u>GGCTCAG</u>	20	GGCAGGCCTA	ACACATGCAA	1638
	AAATTGAAGA	<u>GTTTGATCAT</u>	<u>GGCTCAGATT</u>	GAACGGCTGCC	CCGTCCGGAT	TGTGTACGTT	
	TTTAACCTCT	CAAACACTAGTA	<u>CCGAGTCTAA</u>	CTTGGCACCG			
70			90	100	GGGGGAC	GGGTGAGTAA	
					AGTGGGGAC	<u>GGGTGAGTAA</u>	ER10
130	GTCTGGAA	AACAGGAAGA	<u>AGCTTGCCTTC</u>	TTTGCTGACCG	AACGGTAGCT	AATACCGCAT	
	CAGCTTGCCA	TTGTCCCTCT	TCGAACGAAG	AAACGACTGC	TTGATGACCT	TTATGGCGTA	
190			140	150	160	170	180
	TGTCTGGAA	ACTGCCCTGAT	GGAGGGGGAT	AACTACTGGAA	AACGGTAGCT	AATACCGCAT	
	ACAGACCCCTT	TGACGGACTA	CCTCCCCCTA	TTGATGACCT	TTGATGACCT	TTATGGCGTA	
250			200	210	220	230	240
	AACGTCGCAA	GACCAAAAGAG	GGGGACCCTTTC	GGGGCTCTTG	CCATCGGATG	TGCCCAAGATG	
	TTGCAGCCGT	CTGGTTTCTC	CCCCTGGAAAG	CCCCTGGAAAG	GGTAGCCTAC	ACGGGTCTAC	
310			260	270	280	290	300
	GGATTAGCTA	GTAGGGGGG	TAACGGCTCA	CCTAGGGCGAC	GATCCCCTAGC	TGGTCTGAGA	
	CCTAAATCGAT	CATCCACCCC	ATTGCCGAGT	GGATCCGCTG	CTAGGGATCG	ACCAAGACTCT	

FIG. 88A

370	380	390	400	410	420
GGAAATTGCG	ACAATGGCG	CAAGCCTGAT	GCAGCCATGCC	GGCGTGTATG	AAGAAGGGCT
CCTTATAACG	TGTTACCCGC	GTTGGACTA	CGTCGGTACG	GGCACATAC	TTCTTCCGGGA
430	440	450	460	470	480
TCGGGTGTA	AAGTACTTTC	AGCGGGGAGG	AAGGGAGTAA	AGTTAAATACC	TTTGCTCAT
AGCCCAACAT	TTCATGAAAG	TGCCCCCTCC	TTCCCTCATT	TCAATTATGG	AAACGAGTAA
490	500	510	520	530	540
GACGTTACCC	GCAGAAGAAG	CACCGGCTAA	CTCCGGGCCA	GCAGGCCGGG	TAATACGGAG
CTGCAATTGGG	CGTCTTCTTC	GTGGCCGATT	GAGGCACGGT	CGTCGGGCC	ATTATGCCTC
550	560	570	580	590	600
GGTGCAGCG	TTAATGGAA	TTACTGGGG	TAAAGGGCAC	GCAGGGGGTT	TGTTAACGTCA
CCACGTTCGC	AATTAGCCTT	AATGACCCGC	ATTTCGGCTG	CGTCCGCCAA	ACAAATTCACT
610	620	630	640	650	660
GATGTGAAAT	CCCCGGGCTC	ACCTGGGAA	CTGCATCTGA	TACTGGCAAG	CTTGAGTCTC
CTACACTTTA	GGGGCCCCGAG	TTGGACCCCTT	GACGTAGACT	ATGACCGTTT	GAACTCAGAG
670	680	690	700	710	720
GTAGAGGGGG	GTAGAATTCC	AGGTGTAGCC	GTGAAATGCG	TAGAGATCTC	GAGGAATACC
CATCTCCCC	CATCTTAAGG	TCCACATGCC	CACTTTACGC	ATCTCTAGAC	CTCCTTATGG
730	740	750	760	770	780
GGTGGCGAAG	GGGGCCCCCT	GGACCGAAGAC	TGACCGCTCAG	GTGGGAAAGC	GTGGGAGCA
CCACCGCTTC	GGGGGGGA	CCTGCTTCTG	ACTGGAGTC	CACGGCTTCG	CACCCCTCGT

FIG. 88B

FIG. 88C

1210	ATCATGGCCC	TTA			1220	1230	1240	1250	1260
	ATCATGGCCC	TTACCGA							
	<u>ATCATGGCC</u>	<u>TTACGA</u>	GGCTACACAC	GTGCTACAAT	GGCGCATACA	AAGAGAAAGCG			
	<u>ATCATGGCC</u>	<u>TTACGA</u>	CCGATGTGTC	CACCGATGTTA	CCGGTGTG	TTCCTCTTCCGC			
1270	ACCTCGGAG	AGCAAGCGGA	1280	CCTCATAAAG	TGCCGTGGTAG	TCCGGATTGG	1310	1320	
	TGGAGCGGCTC	TCGTTGCCCT		GGAGTATTTC	ACGCAGCATE	TCAGAACCTG	AGTCTGCACAC		
1330	TCGACTCCAT	GAAGTCGGAA	1340	TGGCTAGTAA	TCGTTGGATCA	GAATGCCACG	1370	1380	
	AGCTGAGGTA	CTTCAGGCCCT		AGCGATCATT	AGCACCTAGT	CTTACGGTGC	<u>CACTTATGCA</u>		
1390	TCCCCGGCCT	TGTACACACC	1400	GCCCCGTCA	CCATGGGAGT	GGGTTGCCAAA	1420	1430	1440
	<u>AGGGGGGGAA</u>	<u>ACATG</u>		CGGGCAGTGT	CCCACGTTT	TCTTCATCCA			
1450	AGCTTAAACCT	TCGGGAGGGC	1460	GCTTACCACT	CCATGGTGA	GAAGTGGGT	1470	1480	1490
	TCGAATTGGA	AGCCCCCTCCG		AACACTAAGT	ACTGACCCCA	CTTCAGGCAT			
1510	CAAGGTAAACC	GTAGGGAAC	1520	ATCACCTCCT	ATCACCTCCT	TA.....			
	CTTCCATTGGC	CATCCCCTTG		GACGCCAAC	CTGGGGTGG	ATAGGGAGGA	AT.....		

EIG
888

1638 (SEQ ID NO:151)	AGAGTTGATCCTGGCTCAG		
E.colirrSE (SEQ ID NO:158)	AAATTGAAGAGTTGATCATGGCTCAGATTGAACGGCTGGCGAGGCCATAACATGCA		
Cam. jejuns (SEQ ID NO:159)	TTTTATGGAGAGTTGATCCTGGCTCAGAGTGAACGGCTGGCGGTGCTTAACATGCA		
Stp. aureus (SEQ ID NO:160)	TTTTATGGAGAGTTGATCCTGGCTCAGGGATGAACGGCTGGCGGTGCTTAACATGCA		
	GGGGACGGG		
ER10 (SEQ ID NO:152)	60	AGTCGAACGGTAACAG	- - - GCTGACCGAGTGGGGACGGG
E.colirrSE	62	AGTCGAACGGAT	- - - GAAAGCTTCTAGCTAGAAGTGA
Cam. jejuns	61	AGTCGGAGCGAA	- - - AGCTGGTCTGATG
Stp. aureus			- - - AGCGGGGGACGGG
ER10	114	TGAGTAATGTCTGGGA	= AACTGCCTGATGGAGGGATAACTACTGGAAACGGTAGCTAAATA
E.colirrSE	114	TGAGTAAGGTATAAGTTAATCTGCCCT	= ACACAAGAGGACAAACAGTTGGAAACGGACTGCTAAATA
Cam. jejuns	113	TGAGTAACACGGATAACCTACCTATAAGACTGGGATAACTGGGATAACCTACCTAAATA	= CGGACGAGGAA
Stp. aureus			
ER10	175	CCGCATAAC	- - - GTCGCAAGAC
E.colirrSE	176	CTCTATACTCCTGCTTAACACAAGTTGAGTAGG	- - - GAAAG
Cam. jejuns	176	GAAAG	- - - TTTTT
Stp. aureus	175	CCGGATAATAATTGTAACCCATGGTCAAAGAACGGGT	- - - CTT
			- - - GCTGTCA
ER10	221	CCATCGGATGTCCCCAGATGGGATTAGCTAGGTGGGTAACGGCTCACCTAGGGGACCGA	
E.colirrSE	221	GTGTAGGATGAGACTATAAGTATCAGCTAGTTGGTAAGGTAATGGCTTACCAAGGCTATGA	
Cam. jejuns	229	CTTATAGATGGATCCGGCTGCATTAGCTAGTTGGTAAGGTAACGGCTTACCAAGGCAACGA	
Stp. aureus			
ER10	283	TCCTAGCTGGTCTGAGGGATGACCAACTGGAAACTGAGACACGGCTCACCTAGGCTTACACTGGTCCAGACTGGCTCACACTGGTCCAGACTCCTA	
E.colirrSE	283	GCTTAACCTGGTCTGAGGGATGATCAGTCACACTGGAAACTGAGACACGGTCCAGACTGGCTCACACTGGTCCAGACTGAGACACGGTCCAGACTGGCTCACACTGGTCCAGACTCCTA	
Cam. jejuns			ACTCCTA
Stp. aureus			
1659 (COMPL)			

FIG. 89A

E. coli rrSE 345 CGGAGGCAGCTGGGAATATTGCACAAATGGGCCAAGCCCTGATGCCAGCATGCCGGTG
 Cam. jejuns 345 CGGAGGCAGCTGGGAATATTGCACAAATGGGCCAAGCCCTGACGCCAGCAACGCCGGTG
 Stp. aureus 353 CGGAGGCAGCTGGGAATATTGCCAATGCCAACGGCAGTAGGAGCAACGCCGGTG
 1659 (COMPL) CGGAGGCAGCAG

 E. coli rrSE 407 TATGAAGAAGGCCCTTGGGTAAAGTACTTTCAAGGGGGAGGAA-GGGAGTAAGTTAAAT
 Cam. jejuns 407 GAGGATGACACTTTGGAGCGTAAACTCCTTTCTTAGGAAAG - - - - - AATT
 Stp. aureus 415 AGTGGATGAAGGTCTGGATCGTAAACTCTGTTATTAGGAAAGAACATAATGTTGAAGTAAAC

 E. coli rrSE 468 ACCTTTGCTCATTGACGTTACCCGGCAGAAGGAAGGCCACCGGCTAACTCCGTGCCAGCACGCCGG
 Cam. jejuns 455 C-----TGAACGGTACCTAAGGAATAAGCACCCTAACCTACGCTAACTACGCCAACGGCTAAATCAGAAAGGCCACGGTACCTA
 Stp. aureus 476 -----TGTGGCACATCTGACGGTACCTA

FIG. 89B

89C

E. coli rrSE	840	C ₋ CTTGA ₌ GGCGGTGGCTTCCGGAGCTAACGGCTTAAGTCGACGGGACTGGTACGGTGC
Cam. jejuns	816	G ₋ CTAGT ₋ CATCTCAGTAATTGCAAGCTAACGGCTAACGGTACGGTACGGACCGC
Stp. aureus	848	GT ₋ TTCCGGCTTAGTGCTGCAGCTAACGGCATTAAGCAGCTAACGGC
E. coli rrSE	900	AAGGTTAAACTCAAATGAATTGACGGGGCCGGCACACAAGGGGTGGAGCATGTGGTTAATT
Cam. jejuns	876	AAGATTAAACTCAAAGGAATTAGACGGGGACCCGGCACACAAGGGTGGAGCATGTGGTTAATT
Stp. aureus	909	AAGGTTGAAACTCAAAGGAATTGACGGGGACCCGGCACACAAGGGTGGAGCATGTGGTTAATT
E. coli rrSE	962	CGATGCCAACGCCAAGAACCTTACCTGGTCTTGCACATCCACGGAAAGTTTCAGAGATGAGAAT
Cam. jejuns	938	CGAAGATAACGCCAACCTTACCTGGCTTGCATAAGAACCTTTAGAGATAAGAGG
Stp. aureus	971	CGAAGCAACGCCAACCTTACCAAATCTTGACATCCTTAGAGATAACTCTAGAGATAAGGCC
E. coli rrSE	1024	GTG ₋ CCCTTCGGG ₋ AA ₋ AA ₋ CCGTGAGACAGGTGCTGCATGGCTCAGCTCGTGTGTA
Cam. jejuns	1000	GTGCTAGCTTGGCTAGAA ₋ CTTAGAGACAGGTGCTGCACGGCTCGTGTGTA
Stp. aureus	1033	TTCC ₋ CCCTTCGGG ₋ GGACAAAGTGAAGGATGGCTCAGCTCGTGTGCA
SB-1		GCAACGGAGCGCAACCC
E. coli rrSE	1081	AATGTTGGGTTAAGTCCCCTTATCCTTGTGCCCCAGCCAGCTTACGGTTGCTAACGGT
Cam. jejuns	1061	GATGTTGGGTTAAGTCCCCTGCAACCCAGCTATTAGTTAGCTTAAAGCTTAAAGCTTAAAGT
Stp. aureus	1092	GATGTTGGGTTAAGTCCCCTGCAACCCAGCTTAAAGCTTAAAGCTTAAAGT

FIG. 89D

<i>E. coli</i> rrSE	1389	CTTGTACACCCGCCCGTCACACCATTGGAGTAGGTTAACCT	
<i>Cam. jejuns</i>	1368	CTTGTACTCACCGCCCGTCACACCATTGGAGTAGGTTAACCT	
<i>Stp. aureus</i>	1399	ATTGTACACCCGCCCGTCACACCATTGGAGTAGGTTAACCT	
	1743 (compl)	CTTGTAC	
<i>E. coli</i> rrSE	1451	TCG_GGAGGGCGCTTACCACTTTGTGATTCATGACTGGGGTGAAGTCGTAACAAGGTAA	C
<i>Cam. jejuns</i>	1427	AC_-T-AAGTTACCGGTCCACAGTGGAAATCAGCGACTGGGGTGAAGTCGTAACAAGGTAA	C
<i>Stp. aureus</i>	1461	TTTAGGAGCTAGCCGTGGGACAAATGATTGGGTGAAGTCGTAACAAGGTAA	C
<i>E. coli</i> rrSE	1512	TAGGGAACCTGGGGTTGGATCACCTCCCTA---	C
<i>Cam. jejuns</i>	1485	TAGGAGAACCTGGGGTTGGATCACCTCCCT---	C
<i>Stp. aureus</i>	1523	TATCGGAAGGTGGGCTGGATCACCTCCCTTCT-	C

FIG. 89F

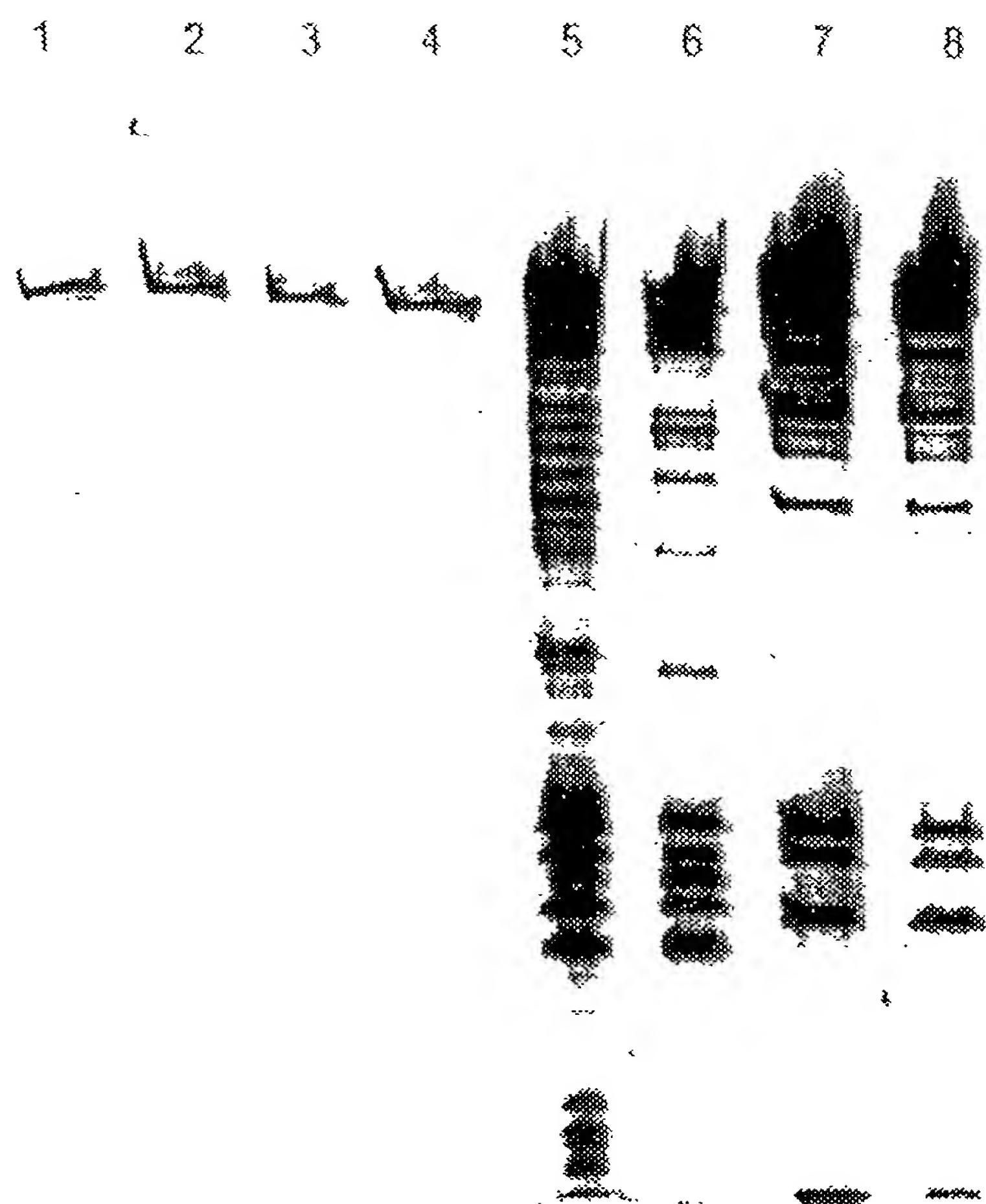


FIG. 90

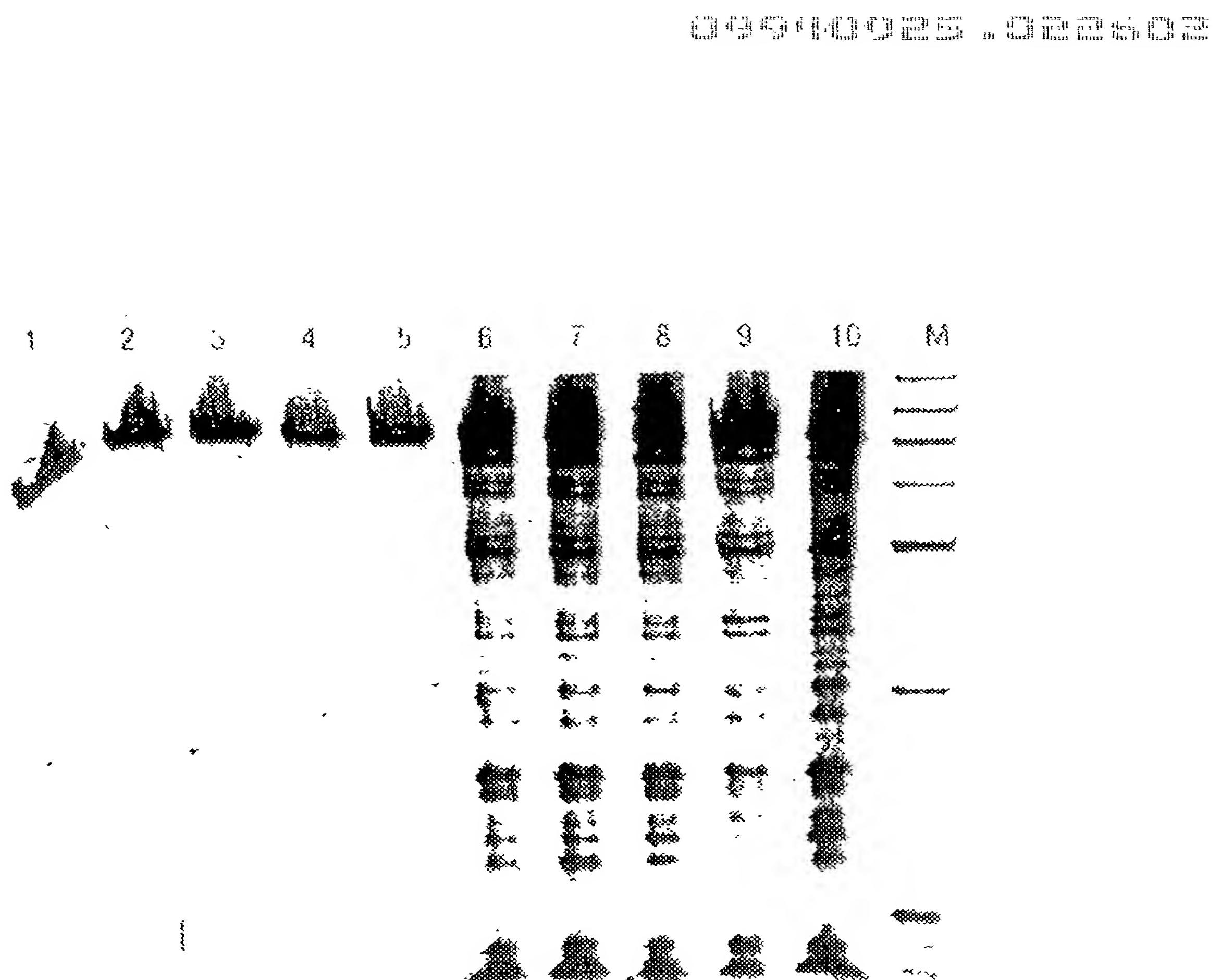


FIG. 91A

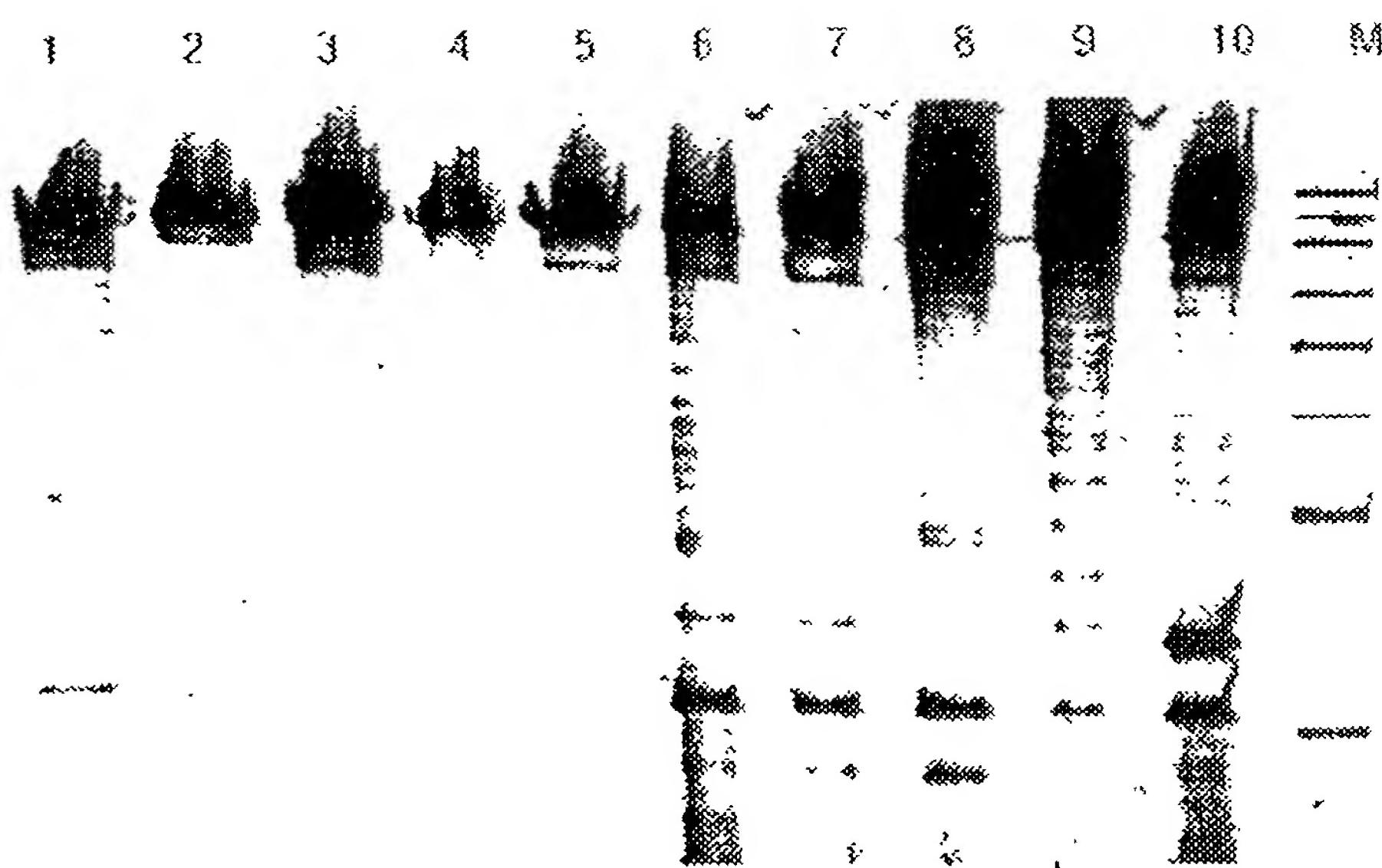


FIG. 91B

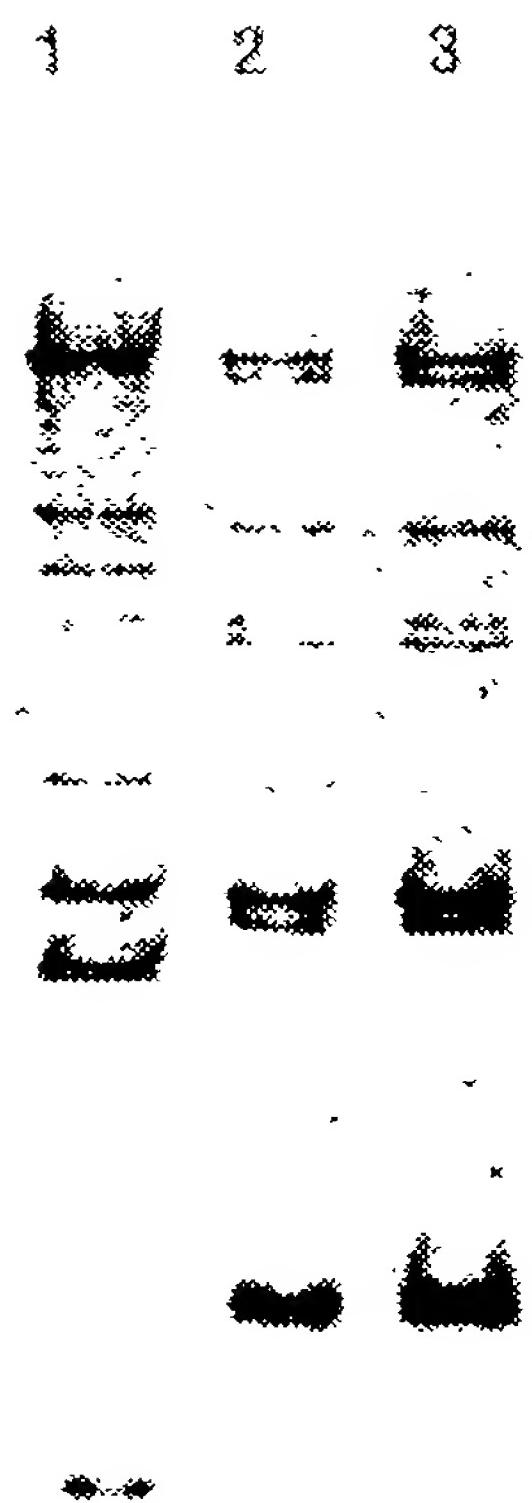


FIG. 92

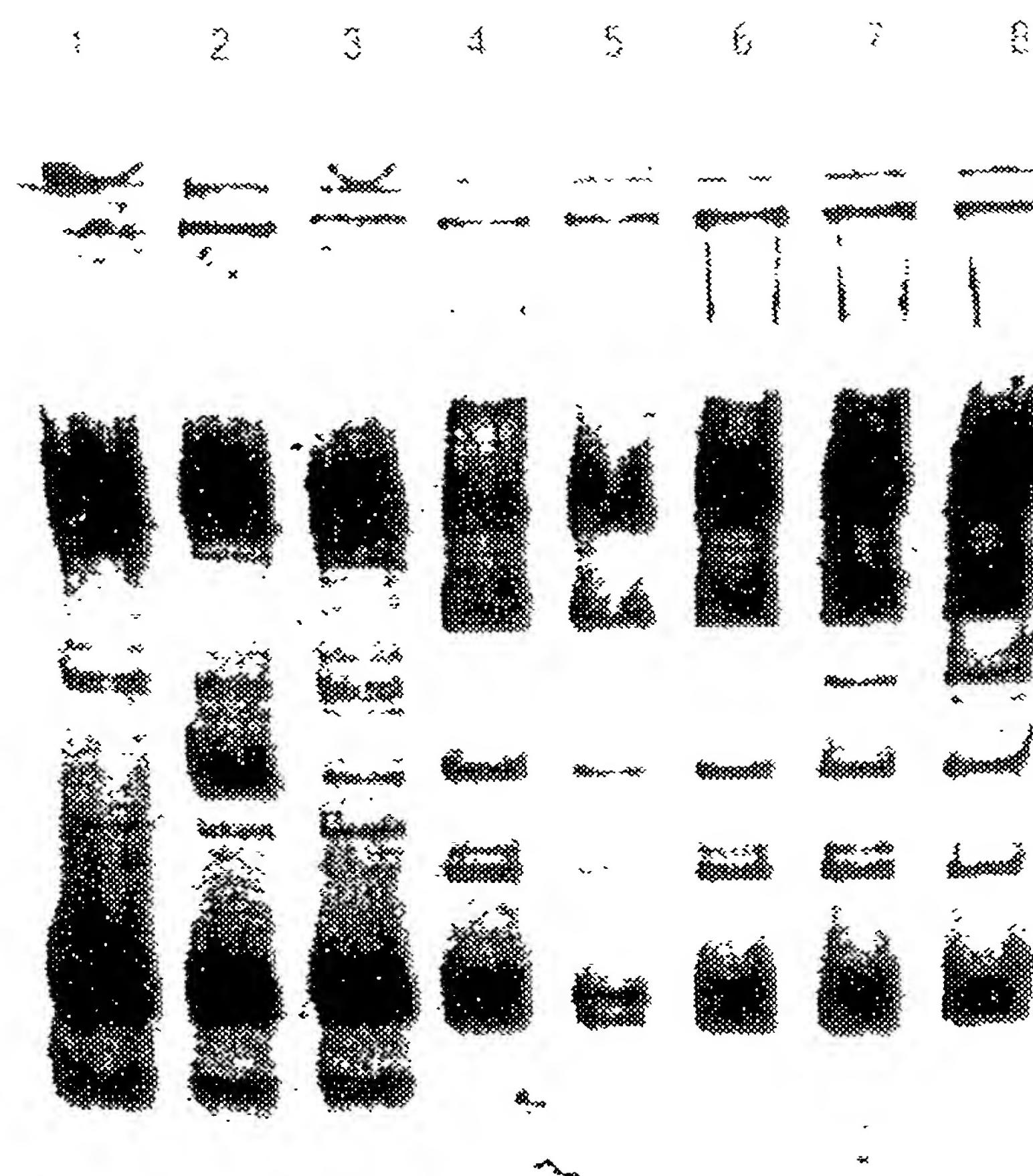


FIG. 93

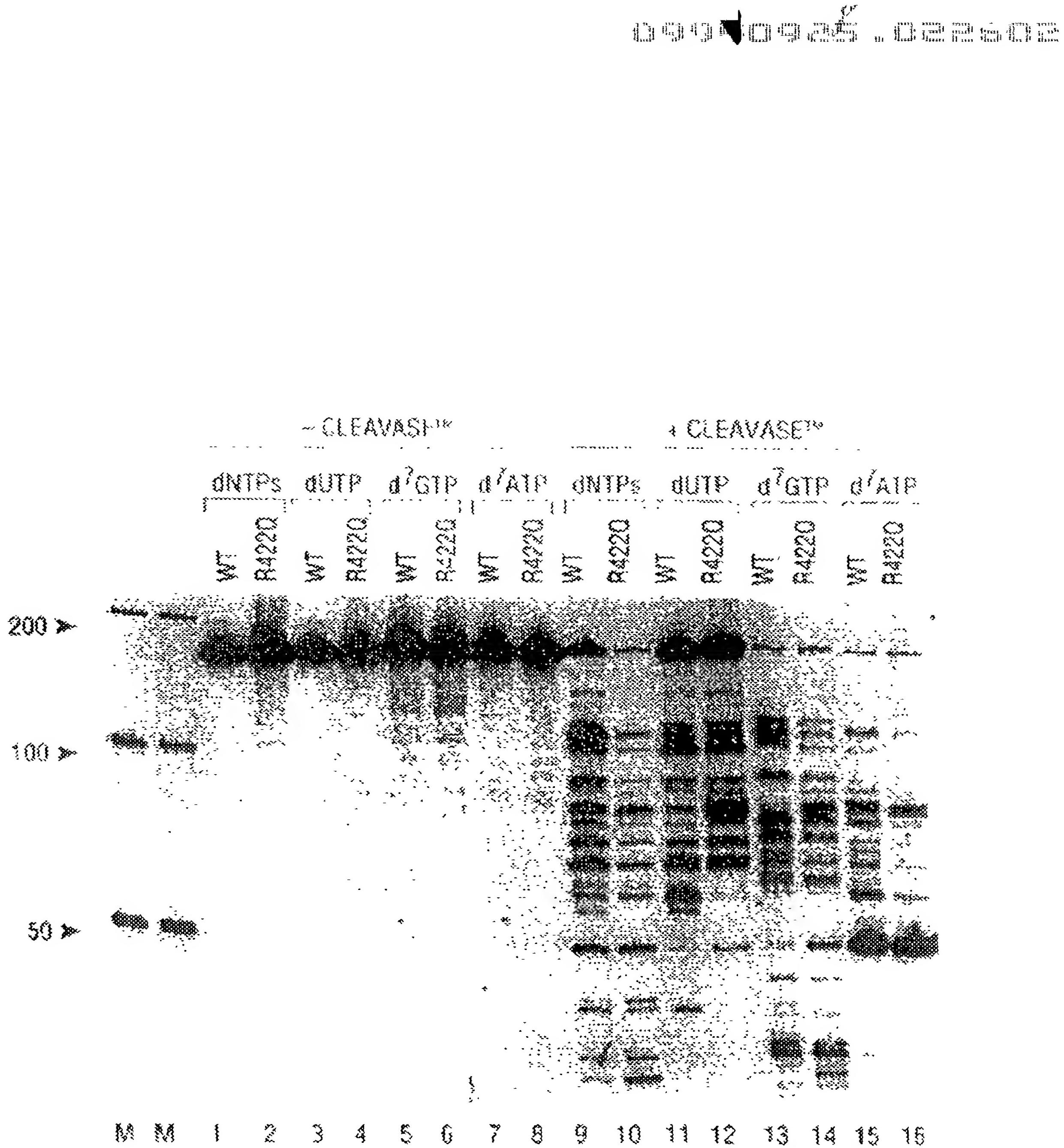


FIG. 94